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OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 22:32:20 ; Search time 13960 Seconds  
(without alignments)  
6951.179 Million cell updates/sec

Title: US-09-940-921B-1

Perfect score: 2052  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba.\*

2: gb\_btg.\*

3: gb\_in.\*

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5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

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13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2052	100.0	2052	6	AX394703 Sequence
2	2052	100.0	2240	6	AX394707 Sequence
3	1967	95.9	2949	9	BC063885 Homo sapi
4	1868	91.0	1965	6	AX394705 Sequence
5	1654	80.6	2370	6	AR269117 Sequence
6	1654	80.6	2370	6	AR487609 Sequence
7	1469.6	71.6	1947	6	AX166554 Sequence
8	1359.8	66.3	1896	6	AX659636 Sequence
9	1359.8	66.3	1918	6	AX659639 Sequence
10	797.2	38.8	1884	6	CO732078 Sequence
11	788.8	38.4	3635	6	CO843384 Sequence
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23	368	17.9	5532	6	AR338754 Sequence
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ALIGNMENTS

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ACCESSION AX394703  
VERSION AX394703.1 GI:21065806  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
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AUTHORS Friddle,C.J., Hilburn,E., Nepomnichy,B. and Hu,Y.  
TITLE Human kinase proteins and polynucleotides encoding the same  
JOURNAL Patent: WO 021855-A 1 07-MAR-2002;  
Lexicon Genetics Incorporated (US)  
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## RESULT 2

AX394707

LOCUS

DEFINITION

AX394707

ACCESSION

AX394707.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX394707 Sequence 5 from Patent WO0218555.

AX394707 AX394707.1 GI:21065808

Homo sapiens (human)

Homo sapiens

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

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Friddle, C.J., Hilbun, E., Nepomnich, B. and Hu, Y.

Human kinase proteins and polynucleotides encoding the same

Patent: WO 0218555-A 5 07-MAR-2002;

Lexicon Genetics Incorporated (US)

Location/Qualifiers

1. .2240

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Lexicon Genetics Incorporated (US)

Location/Qualifiers

/db\_xref="taxon:9606"

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LOCUS AX394705 1965 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 3 from Patent WO0218555.
ACCESSION AX394705
VERSION AX394705.1 GI:21065807
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Friddle, C.J., Hilbun, E., Nepomnichy, B. and Hu, Y.
AUTHORS Human kinase proteins and polynucleotides encoding the same
TITLE Patent: WO 021855-A 3 07-MAR-2002;
JOURNAL Lexicon Genetics Incorporated (US)
FEATURES
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1. 1965
/organism="Homo sapiens"
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KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 2370)
AUTHORS	Webster M., Yan, C., Di Francesco, V., and Beasley, E.
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
JOURNAL	Patent: US 650656-A 1 31-DEC-2002;
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VERSION          AR487609.1  GI:47252885
KEYWORDS
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ORGANISM         Unclassified.
REFERENCE        1 (bases 1 to 2370)
AUTHORS          Webster, M., Yan, C., Di Francesco, V. and Beasley, E.
TITLE            Isolated human kinase proteins
JOURNAL          Patent: US 6706510-A 1 16-MAR-2004;
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 LOCUS  
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 ACCESSION AX166554  
 VERSION AX166554.1 GI:14546899  
 KEYWORDS  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE  
 1 Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,  
 Flanagan, P. and Clary, D.S.  
 TITLE Novel human protein kinases and protein kinase-like enzymes  
 JOURNAL Patent: WO 0138503-A 45 31-MAY-2001;  
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 QY 421 ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGCTTGAATTAATTCATGAACTT 480  
 Db 421 ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGCTTGAATTAATTCATGAACTT 480  
 QY 481 GCTCGAATTTGATTTGGAACACCTTACTACCTGTCCACAGATCTGTCAGAAATTAACCC 540  
 Db 481 GCTCGAATTTGATTTGGAACACCTTACTACCTGTCCACAGATCTGTCAGAAATTAACCC 540

QY 541 TACAACATAAAGCGGATATTTGGTCTCTTGGCTGTGCTTATATAGCTGTGCACACTT 600  
 Db 541 TACAACATAAAGCGGATATTTGGTCTCTTGGCTGTGCTTATATAGCTGTGCACACTT 600  
 QY 601 AAACATCCTTTTGGAGGTAAACAACTTACAGCAGCTGTTCTGAGATTTGTCAAGCACAT 660  
 Db 601 AAACATCCTTTTGGAGGTAAACAACTTACAGCAGCTGTTCTGAGATTTGTCAAGCACAT 660  
 QY 661 TTTGCCCAATATCTCCGGGGTTTTCTCGTGGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 Db 661 TTTGCCCAATATCTCCGGGGTTTTCTCGTGGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 QY 721 CAAGTATCTCTCCAGAGACCGACCATCAATAAATTCATTTTGAAGAGCCCTTTTAGAG 780  
 Db 721 CAAGTATCTCTCCAGAGACCGACCATCAATAAATTCATTTTGAAGAGCCCTTTTAGAG 780  
 QY 781 AATCTTATTCCTCAATATTTGATCTCTGAGTGTATTCAGGAAGATTCAGTCAATGCTT 840  
 Db 781 AATCTTATTCCTCAATATTTGATCTCTGAGTGTATTCAGTCAATGCTTCAATGCTT 840  
 QY 841 ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTCGGAAGGTGGTCCAGAACTGTAAA 900  
 Db 841 ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTCGGAAGGTGGTCCAGAACTGTAAA 900  
 QY 867 -----GGTGACTGTTGGATTTTGGCAGAGATTTGGGTTCAGGTCCTTG 867  
 QY 901 ATACAAAAGTGAATTCAGGGAAGTGCACCAAGATCAAGATATCTGTGCCAAT 960  
 Db 901 ATACAAAAGTGAATTCAGGGAAGTGCACCAAGATCAAGATATCTGTGCCAAT 960  
 QY 927 ACACGTGTGTTGGTGTAGGTCAGCCACTGCACCCAGCTGTATTTATGGTGTAAAA 927  
 Db 927 ACACGTGTGTTGGTGTAGGTCAGCCACTGCACCCAGCTGTATTTATGGTGTAAAA 927  
 QY 961 AARAGGAATGATATATGATAGAAATGAATGGAGACCAAGCTGGAGCCAGAGGCC 1020  
 Db 961 AARAGGAATGATATATGATAGAAATGAATGGAGACCAAGCTGGAGCCAGAGGCC 1020  
 QY 948 AACATCCCTCTGTTTCTT----- 948  
 Db 948 AACATCCCTCTGTTTCTT----- 948  
 QY 1021 AGATCTATAAAATGATAGAAAGACCCAAATTTGCTGCTGTCTGTGACATTTATGATTAT 1080  
 Db 949 ---CAGATAAAATGATAGAAAGACCCAAATTTGCTGCTGTCTGTGACATTTATGATTAT 1005  
 QY 1081 TATTTATGCTCAACTGTGATATGCTGAGGAGGAGCCCAAAACCAAGTTATCAACCTTAT 1140  
 Db 1081 TATTTATGCTCAACTGTGATATGCTGAGGAGGAGCCCAAAACCAAGTTATCAACCTTAT 1065  
 QY 1141 CCTCAAGAAATATCTGGAGTTGAGGATTACGGTCAGGAAACGAGGATGTGTCATCCCCA 1200  
 Db 1066 CCTCAAGAAATATCTGGAGTTGAGGATTACGGTCAGGAAACGAGGATGTGTCATCCCCA 1125  
 QY 1201 AGTCAATGGCTGTGATGATACCTTTCAGAGAAATTTGAAGCTCAACAAATATAGTTGAAA 1260  
 Db 1126 AGTCAATGGCTGTGATGATACCTTTCAGAGAAATTTGAAGCTCAACAAATATAGTTGAAA 1185  
 QY 1261 GTGGAGAGCAATTTGGGTCTTTCGTCATCTTCTGCGAGCCAAATACACCCAGAGCAA 1320  
 Db 1186 GTGGAGAGCAATTTGGGTCTTTCGTCATCTTCTGCGAGCCAAATACACCCAGAGCAA 1245  
 QY 1321 GAGCTAAGAAATATGAGAGAGCCTTAGATTCCAGAGCTGCCATTTAGGAAAAACGAA 1380  
 Db 1246 GAGCTAAGAAATATGAGAGAGCCTTAGATTCCAGAGCTGCCATTTAGGAAAAACGAA 1305  
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 Db 1306 ATGAGGAAACAGGATATTTGGAGGAGTGGGAGAGAAACCCAGTACCAATGAC 1365  
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 Db 1366 ATGAGGAAATTTAGAAAGAGATGGGAGAGAAACCCAGTACCAATGAC 1402  
 QY 1501 AAAAACTTATTTGGTGAAGAGATTAACCTCCCTGTCATCAAGATGCTGTAGGGAGAA 1560  
 Db 1403 ----- 1402  
 QY 1561 GCACCTGTGAGGACATTTGAAAAAGACTTGAACAAATGAGGCTTCAGAACACAAAGGAA 1620  
 Db 1403 -----AGACATTTGAAAAAGACTTGAACAAATGAGGCTTCAGAACACAAAGGAA 1452  
 QY 1621 AGTAAAAATCCAGAACAGAAATATAAGCTTAAGAGGGGGTAAAAATTTGAAATTAATTTA 1680

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Db      1453 AGTAAATCCAGAACAGAAATATTAAGCTAAGAGGGGTAAATTTGAATTAATTTA 1512
Qy      1681 GACAAATGATTTCTGATGAAACATCTCTCAAGAGGAGGCAATGATATACCAAAAT 1740
Db      1513 GACAAATGATTTCTGATGAAACATCTCTCAAGAGGAGGCAATGATATACCAAAAT 1572
Qy      1741 GAACTTTGACCTTTGAGGTGGATGAAGTTTAAAGTAATGATGTTAAAGGAGCAT 1800
Db      1573 GAACTTTGACCTTTGAGGTGGATGAAGTTTAAAGTAATGATGTTAAAGGAGCAT 1632
Qy      1801 GGAGATTATACAGACAAAGCATTTGAAAAAATCTCACTGCCAGAGCAGGGCTTTTCCACG 1860
Db      1633 GGAGATTATACAGACAAAGCATTTGAAAAAATCTCACTGCCAGAGCAGGGCTTTTCCACG 1692
Qy      1861 CAGACTGTAGCTGTGTGGGAAACAGGAGGAGTGGGATGAGAGCGCCTCAGACTCTG 1920
Db      1693 CAGACTGTAGCTGTGTGGGAAACAGGAGGAGTGGGATGAGAGCGCCTCAGACTCTG 1752
Qy      1921 CTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCAGCGGGCCCTGACAGTG 1978
Db      1753 CTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCAGCGGGCCCTGACAGTG 1810

RESULT 8
AX659636      1896 bp      DNA      linear      PAT 22-MAR-2003
LOCUS      AX659636
DEFINITION      Sequence 1 from Patent WO03000903.
ACCESSION      AX659636
VERSION      AX659636.1      GI:29161818
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Xiao, Y.
TITLE      Regulation of human nek-like serine/threonine protein kinase
JOURNAL      Patent: WO 03000903-A 1 03-JAN-2003;
              Bayer Aktiengesellschaft (DE)
FEATURES
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ORIGIN
Query Match      66.3%; Score 1359.8; DB 6; Length 1896;
Best Local Similarity 84.5%; Pred No. 2.6e-309;
Matches 1673; Conservative 0; Mismatches 82; Indels 224; Gaps 4;

Qy      1      ATGGATAAGTACGATGTGATTAAGCCATCGGGCAAGGTGCTTCGGGAAAGCATCTTA 60
Db      1      ATGGATAAGTACGATGTGATTAAGCCATCGGGCAAGGTGCTTCGGGAAAGCATCTTA 60
Qy      61      GCTAAGGGAATCAGATAGCAGACCTGTGCTATAAGAGATCAATTTTGAAGAAGTG 120
Db      61      GCTAAGGGAATCAGATAGCAGACCTGTGCTATAAGAGATCAATTTTGAAGAAGTG 120
Qy      121      CCATACAGAAAAAGAGCTTCAAGAAAGAGTGTATTTCTTGGAAAGATGAAACAT 180
Db      121      CCATACAGAAAAAGAGCTTCAAGAAAGAGTGTATTTCTTGGAAAGATGAAACAT 180
Qy      181      CCCACATGTAGCTTCTTCAATTCATTTCAAGAGATGCGAGCTGTTTATTGTAATG 240
Db      181      CCCACATGTAGCTTCTTCAATTCATTTCAAGAGATGCGAGCTGTTTATTGTAATG 240
Qy      241      GAATATTGTGAGGAGGATCTCATGAAAGAGATCAATAGACACCGGGGTGTGTTATTT 300
Db      241      GAATATTGTGAGGAGGATCTCATGAAAGAGATCAATAGACACCGGGGTGTGTTATTT 300
Qy      301      AGTGAAGATCAGATCCTCGGTGGTTTGTACAGATTTCTTAGACTAAACATATTCAT 360

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Db      301      AGTGAAGATCAGATCCTCGGTGGTTTGTACAGATTTTCTTAGGACTAAACATATTCAT 360
Qy      361      GACAGGAAGATATTACAGAGGACATATAAAGCTCAGAACATTTTCTTAGCAGAACGGA 420
Db      361      GACAGGAAGATATTACAGAGGACATATAAAGCTCAGAACATTTTCTTAGCAGAACGGA 420
Qy      421      ATGCTGGCAAAAGCTTGGGACCTTTGGTATAGCAAGAGCTCTCAATAAATTCATGGAACCT 480
Db      421      ATGCTGGCAAAAGCTTGGGACCTTTGGTATAGCAAGAGCTCTCAATAAATTCATGGAACCT 480
Qy      481      GCTCGAACTTGTATTGGAACACCTTACTACCTGTGCCAGAGATCTGTCAGAAATTAACCC 540
Db      481      GCTCGAACTTGTATTGGAACACCTTACTACCTGTGCCAGAGATCTGTCAGAAATTAACCC 540
Qy      541      TACAACAATAAAGGATATTGGTCTCTTGGCTGTGTCTTATATAGCTCTGACACCTT 600
Db      541      TACAACAATAAAGGATATTGGTCTCTTGGCTGTGTCTTATATAGCTCTGACACCTT 600
Qy      601      AAACATCTTTTGGAGGTAACTTACAGAGCTGGTTCTCAAGATTTGTCAAGACAT 660
Db      601      AAACATCTTTTGGAGGTAACTTACAGAGCTGGTTCTCAAGATTTGTCAAGACAT 660
Qy      661      TTGCCCCGAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
Db      661      TTGCCCCGAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720
Qy      721      CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTAGAG 780
Db      721      CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTAGAG 780
Qy      781      AATCTTATTTCCAAATATTTGACTCTCTGAGCTCANTTCAGGAAGATTCAGTCACATGCTT 840
Db      781      AATCTTATTTCCAAATATTTGACTCTCTGAGCTCANTTCAGGAAGATTCAGTCACATGCTT 840
Qy      841      ATATGAGAGCAGGAGCGGCTCTCGACATGCTGGGAAGGTGGTCCAGAAAGTGA-A 899
Db      841      ATATGAGAGCAGGAGCGGCTCTCGACATGCTGGGAAGGTGGTCCAGAAAGTGA-A 899
Qy      900      ATATAAAAAGTGAGATTCAGGGAAGAGTGCCCAACAAGATCAAGGATATCTGTCGCAAT 959
Db      901      GGTGTGAGGAGTGGGCTCTCAAGGGCTTGGGAGCTCTGCTCTGAGGCTTTGCGAGGCTA 960
Qy      960      TAAAGGAATGCTATATTTCCATAGAAATGAATGGAGACCACCGCTGGAGCCCAAGGC 1019
Db      961      CAGCCCCCTGGGCTGCTCTCAGAG-----CTGCTGTGTAGTGTCTCGGCT 1007
Qy      1020      CAGATCTATAAAAATGATAGAAAGACCCAAAATGCTGCTGTCTGTGGACATTTATGATTA 1079
Db      1008      TTTCCAGATAAAAATGATAGAAAGACCCAAAATGCTGCTGTCTGTGGACATTTATGATTA 1067
Qy      1080      TTATATGCTCAACTTGATATCTGAGGAGGAGAGCCCAAAAGCTTATCACCCCTAT 1139
Db      1068      TTATATGCTCAACTTGATATCTGAGGAGGAGAGCCCAAAAGCTTATCACCCCTAT 1127
Qy      1140      TCCTCAAGAAAATACTTGGAGTTGAGATTAACGGTTCAGGAAACGAGGCATGTCCTCCCT 1199
Db      1128      TCCTCAAGAAAATACTTGGAGTTGAGATTAACGGTTCAGGAAACGAGGCATGTCCTCCCT 1187
Qy      1200      AGTCAATGCCCTGTGAGTACCTTCAGAGAAAATTTGAGCTCAACATATAAGTTGAA 1259
Db      1188      AGTCAATGCCCTGTGAGTACCTTCAGAGAAAATTTGAGCTCAACATATAAGTTGAA 1247
Qy      1260      AGTGAAGAGCAGCAATTTGGGTCTTCTGCTCCATCTTCTCGGAGCCCAATTTACAACAGAGACA 1319
Db      1248      AGTGAAGAGCAATTT----- 1262
Qy      1320      AGAGCTAAGAAGTAATGAGAGAGAGCGCTAGATTTCCAGGAGCTGCCATTTAGGAAAAACA 1379
Db      1263      ----- 1262
Qy      1380      AATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAATACGCCAACAGTACCAATGA 1439
Db      1263      -----GGAATATTGGAAGCAGTTAGAGGAATACGCCAACAGTACCAATGA 1310

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QY 1440 CATGAAGAAATTTAGAAAGAGATGGGAGAGAAACAGAGGAGAACTCAAAAATAGTCA 1499
Db 1311 CATGAAGAAATTTAGAAAGAGATGGGAGAGAACAG----- 1348
QY 1500 TAAACCTATTGGTGAAGAGAGTAACTGCTGTCCATCAAGATGCATCTGAGGGAGA 1559
Db 1349 ----- 1348
QY 1560 AGCACCTGTGCAGGACATTGAAAAAGACTTGAACAAATGAGGCTTCAGAACACAAAGGA 1619
Db 1349 -----AGGACATTGAAAAGACTTGAACAAATGAGGCTTCAGAACACAAAGGA 1397
QY 1620 AAGTAAAAATCCAGAACAGAAATATAAGCTAAGAGGGGGTAAAAATTGAAATTTAAATTT 1679
Db 1398 AAGTAAAAATCCAGAACAGAAATATAAGCTAAGAGGGGGTAAAAATTGAAATTTAAATTT 1457
QY 1680 AGACAAATGATTTCTGATGAACAAATCTCTCCAGAGGAGAGGCAATGGATATACCAA 1739
Db 1458 AGACAAATGATTTCTGATGAACAAATCTCTCCAGAGGAGAGGCAATGGATATACCAA 1517
QY 1740 TGAACCTTTGACCTTTGAGGATGGCATGAAGTTTAAAGGAATATGAATGTGTAAGGAGCA 1799
Db 1518 TGAACCTTTGACCTTTGAGGATGGCATGAAGTTTAAAGGAATATGAATGTGTAAGGAGCA 1577
QY 1800 TGGAGATTTACAGACAAAGCATTTGAAAAAATTCATGCCCCAGAGAGGGTTTTCAC 1859
Db 1578 TGGAGATTTACAGACAAAGCATTTGAAAAAATTCATGCCCCAGAGAGGGTTTTCAC 1637
QY 1860 CGAGACTGTAGTGTCTGGGAAAACAGAGGAGGAGTGGGATGAGAGAGCGCTTCAGACTCT 1919
Db 1638 CGAGACTGTAGTGTCTGGGAAAACAGAGGAGGAGTGGGATGAGAGAGCGCTTCAGACTCT 1697
QY 1920 GTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCCCAGGGGCTGACAGTG 1978
Db 1698 GTGCAGATGATGGCAGTGGCCGACATCACCTCCACCTGCCCCAGGGGCTGACAAATG 1756

RESULT 9
AX659639 LOCUS 1918 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 4 from Patent WO03000903.
ACCESSION AX659639
VERSION AX659639.1 GI:29161819
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xiao, Y.
TITLE Regulation of human nek-like serine/threonine protein kinase
JOURNAL Patent: WO 03000903-A 4 03-JAN-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
    Location/Qualifiers
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ORIGIN
Query Match 66.3%; Score 1359.8; DB 6; Length 1918;
Best Local Similarity 84.5%; Pred. No. 2.6e-309;
Matches 1673; Conservative 0; Mismatches 82; Indels 224; Gaps 4;

QY 1 ATGGATAAGTACGATGTGATTAAGGCCATCGGCGAGGTGCCTTCGGGAAGCATACTTA 60
Db 23 ATGGATAAGTACGATGTGATTAAGGCCATCGGCGAGGTGCCTTCGGGAAGCATACTTA 82
QY 61 GCTAAGAGGAATTCAGATAGCAAGCACTGTGTATATAAGAGATCAATTTTGAAGAATG 120
Db 83 GCTAAGAGGAATTCAGATAGCAAGCACTGTGTATATAAGAGATCAATTTTGAAGAATG 142
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QY 121 CCCATACAGAAAAAGAGCTTCAAGAAAAAGAGTGAATCTTCTGAAAAAGATGAACAT 180
Db 143 CCCATACAGAAAAAGAGCTTCAAGAAAAAGAGTGAATCTTCTGAAAAAGATGAACAT 202
QY 181 CCCAACATTTGAGCCTTCTTCAATTCATTTCAAGAGAAATGGCAGGCTGTTTATGTAAATG 240
Db 203 CCCAACATTTGAGCCTTCTTCAATTCATTTCAAGAGAAATGGCAGGCTGTTTATGTAAATG 262
QY 241 GAATATTGTGATGAGGGGATCTCATGAAAAAGGATCAATAGACAAACGGGGTGTGTTATTT 300
Db 263 GAATATTGTGATGAGGGGATCTCATGAAAAAGGATCAATAGACAAACGGGGTGTGTTATTT 322
QY 301 AGTGAAGATCAGATCTCTCGGTTGGTTGTACAGATTTCTCTAGAGCTTAAACATATTCAT 360
Db 323 AGTGAAGATCAGATCTCTCGGTTGGTTGTACAGATTTCTCTAGAGCTTAAACATATTCAT 382
QY 361 GACAGGAAGATATTACACAGGAGCATAAAAGCTCAGAACATTTTCTTACGAAAGACGA 420
Db 383 GACAGGAAGATATTACACAGGAGCATAAAAGCTCAGAACATTTTCTTACGAAAGACGA 442
QY 421 ATGTTGCAAAAGCTTTGGGAGCTTTGGTATAGCAAGAGTCTCTGAATTAATTCATGGAACTT 480
Db 443 ATGTTGCAAAAGCTTTGGGAGCTTTGGTATAGCAAGAGTCTCTGAATTAATTCATGGAACTT 502
QY 481 GCTCGAATTTGATTTAGAACACCTTACTACTGCTCCCGAGAGATCTCTCAGAAATAACCC 540
Db 503 GCTCGAATTTGATTTAGAACACCTTACTACTGCTCCCGAGAGATCTCTCAGAAATAACCC 562
QY 541 TACAACAAATAAAACGGATATTGGTCTCTTGGGCTGTCTTATATAGAGCTCTGCACACTT 600
Db 563 TACAACAAATAAAACGGATATTGGTCTCTTGGGCTGTCTTATATAGAGCTCTGCACACTT 622
QY 601 AAACATCTTTTGAAGGTAAACACTTACAGAGCTGTTCTGAGAGATTTGTCAGAGCAAT 660
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QY 661 TTTCCCAATATCTCGGGGTTTTCTCGTGAGCTCCATTCCTTGTATATCTCAGCTCTTT 720
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Db 743 CAAGTATCTCTCGAGACCCGACCAATCCATAAAATTCATTTGAAAAGGCCCTTTTAGAG 802
QY 781 ATCTTTATTTCCCAATATTTGACTCTGAGGTCAATTCAGGAAGATTCAGTCAATGCTT 840
Db 803 ATCTTTATTTCCCAATATTTGACTCTGAGGTCAATTCAGGAAGATTCAGTCAATGCTT 862
QY 841 ATATGACAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAAAGTGA-A 899
Db 863 ATATGACAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGGAAGGTGGTCCAGAGGCATACT 922
QY 900 AATCAAAAAAGTGAGATTCAGGGAAGTGCACCAAGATCAAGATATCTGTGCCAAT 959
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QY 960 TAAAAAGGAATGCTATATTGATAGAAATGAATGGAGACCCAGCTGGAGCCAGAGAGGC 1019
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QY 1020 CAGATCTATAAAATATAGAAAGACCCAAAATTTGCTGTGTCTGTGGAATATATGATTA 1079
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QY 1080 TTATATGCTCACTTCATATGCTGAGGAGAGGCCCAACAAACCAAGTTATCACCCCTAT 1139
Db 1090 TTATATGCTCACTTCATATGCTGAGGAGAGGCCCAACAAACCAAGTTATCACCCCTAT 1149
QY 1140 TCCCTCAAGAAAAATCTAGAGTTAGAGTACGGTTCAGAAAAACGAGGATGGTCCATCCCC 1199
Db 1150 TCCCTCAAGAAAAATCTAGAGTTAGAGTACGGTTCAGAAAAACGAGGATGGTCCATCCCC 1209
QY 1200 AAGTCAATGGCTGCTCAGTACCTTACAGAAAAATTTGAAGCTTCAACATATAAGTTGAA 1259
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Db	769		776
Qy	1327	AGAAAGTAATGGAGAAGACCTTAGATTCCAGGAGCTGCCATTTAGAAAAACGAATGAAG	1386
Db	777	-----	776
Qy	1387	GAACAGGAATATTGGAGACGATTAGAGAAATACGCCAACAGTACCAATGACATGAAA	1446
Db	777	-----GGAATATTGGAGACGATTAGAGAAATACGCCAACAGTACCAATGACATGAAA	831
Qy	1447	GAAATTAGAAGAAGATGGGAGAGAACCCAGAGGAGAACTCAAAAAATAGTCATAAAACC	1506
Db	832	GAAATTAGAAGAAGATGGGAGAGAACCCAGAGGAGAACTCAAAAAATAGTCATAAAACC	891
Qy	1507	TATTTGTGGAAGAAGATTAACCTGCCCTGTCATCAAGATGCATCTGAGGAGAGACACCT	1566
Db	892	TATTTGTGGAAGAAGATTAACCTGCCCTGTCATCAAGATGCATCTGAGGAGAGACACCT	951
Qy	1567	GTGCAGGACATTGAAAAGACTTGAACAACAAATGAGGCTTCAGACACACAAAGGAAAGTAAA	1626
Db	952	GTGCAGGACATTGAAAAGACTTGAACAACAAATGAGGCTTCAGACACACAAAGGAAAGTAAA	1011
Qy	1627	AATCCAGAACAGAAATATAAGCTTAAGAAGGGGTAAAAATTGAAATTAATTTAGACAAA	1686
Db	1012	AATCCAGAACAGAAATATAAGCTTAAGAAGGGGTAAAAATTGAAATTAATTTAGACAAA	1071
Qy	1687	TGATTTCTGATGAACATCCTCCAGAGGAGAGGCAATGGATATACCAATGAACT	1746
Db	1072	TGATTTCTGATGAACATCCTCCAGAGGAGAGGCAATGGATATACCAATGAACT	1131
Qy	1747	TTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAGGAGCATGGAGAT	1806
Db	1132	TTGACCTTTGAGGATGGCATGAAGTTTAAGGAATATGAATGTGTAAGGAGCATGGAGAT	1191
Qy	1807	TATACAGACAAAGCATTTGAAAACTTCATGCCCAGAGCAGGGTTTTCCACGACACT	1866
Db	1192	TATACAGACAAAGCATTTGAAAACTTCATGCCCAGAGCAGGGTTTTCCACGACACT	1251
Qy	1867	GTAGCTGCTGTGGAAACAGAGGACGCTGGATGTGGAGGCGCTCAGACTCTGCTGCAG	1926
Db	1252	GTAGCTGCTGTGGAAACAGAGGACGCTGGATGTGGAGGCGCTCAGACTCTGCTGCAG	1311
Qy	1927	ATGATGGAGTGGCCGACATCACTCCACTGCCCCACGGGGCTGACAGTG	1978
Db	1312	ATGATGGAGTGGCCGACATCACTCCACTGCCCCACGGGGCTGACAGTG	1363
RESULT 11			
Q0843384			
LOCUS	Q0843384	3635 bp	DNA linear PAT 02-AUG-2004
DEFINITION	Sequence 2031 from Patent EP1440981.		
ACCESSION	Q0843384		
VERSION	Q0843384.1	GI:50895171	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.		
TITLE	Full-length human cDNA		
JOURNAL	Patent: EP 1440981-A 2031 28-JUL-2004;		
FEATURES	Research Association for Biotechnology (JP)		
SOURCE	Location/Qualifiers		
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ORIGIN			
Query Match	38.4%	Score 788.8;	DB 6; Length 3635;



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Best Local Similarity 98.4%; Pred. No. 7.6e-131;
Matches 608; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 204 TTCAATTTCAAGAAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCT 263
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QY 201 TTTTCTTACAGAAATGGCAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGGATCT 260
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 264 CATGAAAGGATCAATAGACACGGGGTGTGTTATTAGTAAGATCAGATCCTCGGTTG 323
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 261 CATGAAAGGATCAATAGACACGGGGTGTGTTATTAGTAAGATCAGATCCTCGGTTG 320
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 324 GTTGTGACAGATTCTCTAGGACTAAACATATTCATGACAGGAAGATATTACACAGGA 383
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 321 GTTGTGACAGATTCTCTAGGACTAAACATATTCATGACAGGAAGATATTACACAGGA 380
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 384 CATAAAGGTCAGAACATTTTCTTAGCAAGAACGGAATGGTGGCAAGCTTTGGGACTT 443
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 381 CATAAAGGTCAGAACATTTTCTTAGCAAGAACGGAATGGTGGCAAGCTTTGGGACTT 440
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 444 TGGTATAGCAAGAGTCTCAATAATTCATGGAACCTTGCTGCAACTGTATTGGACACC 503
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 441 TGGTATAGCAAGAGTCTCAATAATTCATGGAACCTTGCTGCAACTGTATTGGACACC 500
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QY 504 TTACTACCTGTCCACAGAGATCTGTGAGAAATAAACCTTACAAATATAAACCGGATATTG 563
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QY 501 TTACTACCTGTCCACAGAGATCTGTGAGAAATAAACCTTACAAATATAAACCGGATATTG 560
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 561 GTCTCTTGCTGTGCTTATATGAGCTCTGCACTTAACATCTCTTTGAGGGTAACAA 620
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QY 624 CTTACAGCAGCTGGTCTCAAGATTGTCAAGCACATTTTGCCCAATATCTCCGGGTT 683
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QY 621 CTTACAGCAGCTGGTCTCAAGATTGTCAAGCACATTTTGCCCAATATCTCCGGGTT 680
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QY 684 TTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTTCAAGTATCTCTCGAGACCGACC 743
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QY 801 TCCTGAGGTCATTCAGGA 818
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RESULT 14
BC053516
LOCUS
DEFINITION Mus musculus expressed sequence BB049667, mRNA (cdna clone
ACCESSION BC053516
VERSION BC053516.1 GI:31565169
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2281)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carrinco,P., Frange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Armstrong,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
```

Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
2 (bases 1 to 2281)  
Strausberg,R.  
Direct Submission  
Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Susan L. Sullivan, PhD.  
cDNA Library Preparation: ResGen, Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.I., Masello,C., Maskeri,B., Mastriopop,S., Thomas,P.J., Touchman,J.W., McDowell,J., Pearson,R., Stantripop,S., Walker,M.A., Wetherby,K.D., Wiggins,L., Teurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 100 Row: d Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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 LDKCISEDTVOENAVDKLNLISFEDGTFQHRCKEHEHEDYDRAFEELGPEAE  
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## misc\_feature

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/note="S TKC; Region: Serine/Threonine protein kinases,

catalytic domain"

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## ORIGIN

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Best Local Similarity	81.0%;	Pred. NO. 2.7e-129;		
Matches 722;	Conservative 0;	Mismatches 156;	Indels 13;	Gaps 2;

  

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 DB 906 CACATGAGAACATGCGCCATTCGCCCCACAGCTTCTGAGAGAGTTAGTCCA 956

## RESULT 15

BC068201

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

JOURNAL

REMARK

COMMENT

BC068201 1745 bp mRNA linear PRI 31-MAR-2004  
 Homo sapiens cDNA clone IMAGE:4771714, partial cds.  
 BC068201  
 BC068201.1 GI:45872598

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1745)

Strausberg, R.L., Fellings, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahney, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1745)

Strausberg, R.

Direct Submission

Submitted (29-MAR-2004) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapps@mail.nih.gov](mailto:cgapps@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,

Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth

Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,

Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,

Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,

Duane Smallos, Jeff Stolt, Miranda Tsai, George Yang, Jacque

Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRL Plate: 51 Row: k Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF

analysis.

Location/Qualifiers

1. .1745

FEATURES

source

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ORIGIN

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Best Local Similarity 66.0%; Pred. No. 9.6e-76;
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

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Job time : 13977 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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6369.165 Million cell updates/sec

Title: US-09-940-921B-1

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	368	17.9	5532	4	US-09-620-312D-245
5	352	17.2	4263	4	US-09-166-350-29
6	238.4	11.6	1846	3	US-09-173-581-15
7	238.4	11.6	1846	3	US-09-420-915-15
8	205.2	10.0	63588	4	US-09-873-404-3
9	205.2	10.0	63588	4	US-10-243-735-3
10	170.2	8.3	2079	4	US-09-992-481-1
11	166.8	8.1	2940	3	US-08-870-529-1
12	166.8	8.1	2940	4	US-09-544-794-1
13	166.8	8.1	3264	3	US-08-870-529-8
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16	131.6	6.4	1938	4	US-10-196-927-1
17	131.6	6.4	2847	4	US-10-196-927-5
18	119.6	5.8	2765	4	US-09-799-451-50
19	108.6	5.3	2119	4	US-09-167-206-1
20	106.8	5.2	906	3	US-09-221-235-3
21	106.8	5.2	906	3	US-09-221-928-3
22	106.8	5.2	906	3	US-09-221-527-3
23	106.8	5.2	906	3	US-09-221-236-3
24	106.8	5.2	906	3	US-09-221-416-3
25	106.8	5.2	906	3	US-09-221-245-3
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43	100	4.9	1060	4	US-10-355-975A-2	Sequence 2, Appli
44	88.6	4.3	7218	1	US-08-232-463-14	Sequence 14, Appli
45	85.2	4.2	4880	3	US-09-031-563-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-873-404-1

; Sequence 1, Application US/09873404

; Patent No. 6500656

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001212-CIP

; CURRENT APPLICATION NUMBER: US/09/873,404

; CURRENT FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2370

; TYPE: DNA

; ORGANISM: Human

US-09-873-404-1

Query Match	80.6%	Score 1654;	DB 4;	Length 2370;
Best Local Similarity	94.5%	Pred. No. 0;		
Matches 1763;	Conservative	0;	Mismatches 10;	Indels 93; Gaps 1;
Qy	1	ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	60	
Db	12	ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	71	
Qy	61	GCTAAAGGGAATCAGATAGCAGCTGTGTCTATAAAGAGATCAATTTTGAAGATG	120	
Db	72	GCTAAAGGGAATCAGATAGCAGCTGTGTCTATAAAGAGATCAATTTTGAAGATG	131	
Qy	121	CCCATACAAGAAAAGAGCTTCAAGAAAAGAGTGTATTTCTTGGAAAAGATGAAACAT	180	
Db	132	CCCATACAAGAAAAGAGCTTCAAGAAAAGAGTGTATTTCTTGGAAAAGATGAAACAT	191	
Qy	181	CCCAACATTGAGCTTCTTCAATTTCAATTTCAAGAGATGCGAGCTGTATTGTAATG	240	
Db	192	CCCAACATTGAGCTTCTTCAATTTCAATTTCAAGAGATGCGAGCTGTATTGTAATG	251	
Qy	241	GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGAACCGGGTGTGTTATTT	300	
Db	252	GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGAACCGGGTGTGTTATTT	311	
Qy	301	AGTGAAGATCAGATCCCTCGGTTGGTTGTACAGATTTCTTAGGACTAAACATATTCAT	360	
Db	312	AGTGAAGATCAGATCCCTCGGTTGGTTGTACAGATTTCTTAGGACTAAACATATTCAT	371	
Qy	361	GACAGGAAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTACCAAGACGGA	420	

Db 372 GACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTCTTTAGCAAGAACGGA 431  
QY 421 ATGGTGGCAAGCTTTGGGACCTTTGGTATAGCAAGAGTCTTGAATAATTCATGGAACCTT 480  
Db 432 ATGGTGGCAAGCTTTGGGACCTTTGGTATAGCAAGAGTCTTGAATAATTCATGGAACCTT 491  
QY 481 GTCGAACCTTGTATGGGAACACCTTACTACTCTGTGCTCCAGAGATCTGTGAGAAATAAACCC 540  
Db 492 GTCGAACCTTGTATGGGAACACCTTACTACTCTGTGCTCCAGAGATCTGTGAGAAATAAACCC 551  
QY 541 TACAACAATAAAGCGATATTTGGTCTCTTGGCTGTGCTTATATAGCTCTGACACATTT 600  
Db 552 TACAACAATAAAGCGATATTTGGTCTCTTGGCTGTGCTTATATAGCTCTGACACATTT 611  
QY 601 AAACATCTCTTTGAGGGTAACAACCTTACAGCAGCTGGTCTTGAAGATTTGTCAAGCACAT 660  
Db 612 AAACATCTCTTTGAGGGTAACAACCTTACAGCAGCTGGTCTTGAAGATTTGTCAAGCACAT 671  
QY 661 TTTGGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
Db 672 TTTGGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 731  
QY 721 CAAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGGCCCTTTTATAG 780  
Db 732 CAAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGGCCCTTTTATAG 791  
QY 781 AATCTTATCTCCCAATATTTGACTCTGAGTGCATTCAGGAAGATTCAGTCAATGCTT 840  
Db 792 AATCTTATCTCCCAATATTTGACTCTGAGTGCATTCAGGAAGATTCAGTCAATGCTT 851  
QY 841 ATATGACAGCAGGAGCGCAGCTTCTCGAATGCTGGGAAGGTGGTCCAGAAGTGA 900  
Db 852 ATATGACAGCAGGAGCGCAGCTTCTCGAATGCTGGGAAGGTGGTCCAGAAGTGA 911  
QY 901 ATACAAAAGTGAGATTTCCAGGGAAGTGCACCAAGATCAAGATATCTGTGCCAAT 960  
Db 912 ATACAAAAGTGAGATTTCCAGGGAAGTGCACCAAGATCAAGATATCTGTGCCAAT 971  
QY 961 AAAGGAATGCTATATTGCATAGAAATGAATGGAGACCAACAGCTGGAGCCCAAGGCC 1020  
Db 972 AAAGGAATGCTATATTGCATAGAAATGAATGGAGACCAACAGCTGGAGCCCAAGGCC 1031  
QY 1021 AGATCTATAAAATGATAGAAAGCCCAAAATTTGCTGTCTGTGGACATTTATGATAT 1080  
Db 1032 AGATCTATAAAATGATAGAAAGCCCAAAATTTGCTGTCTGTGGACATTTATGATAT 1091  
QY 1081 TATTATGCTCAACTTGATATGCTGAGGAGGAGGCCCAACCAAGTTATCACCTTAT 1140  
Db 1092 TATTATGCTCAACTTGATATGCTGAGGAGGAGGCCCAACCAAGTTATCACCTTAT 1151  
QY 1141 CCTCAAGAAAATPACTGGAGTTGAGATTTACGGTTCAGGAAACGAGGCATGTCCTCCCA 1200  
Db 1152 CCTCAAGAAAATPACTGGAGTTGAGATTTACGGTTCAGGAAACGAGGCATGTCCTCCCA 1211  
QY 1201 AGTCAATGGCTGTGAGTACCTTCAGAGAAAATTTGAAGCTCAACATATAGTTGAAA 1260  
Db 1212 AGTCAATGGCTGTGAGTACCTTCAGAGAAAATTTGAAGCTCAACATATAGTTGAAA 1271  
QY 1261 GTGGAGAGCAATTTGGGTCTTGGTCTTCTGCTCCATCTTCTGCGGAGCAAAATTAACAACAGAGACAA 1320  
Db 1272 GTGGAGAGCAATTTGGGTCTTGGTCTTCTGCTCCATCTTCTGCGGAGCAAAATTAACAACAGAGACAA 1331  
QY 1321 GAGCTAAGAGTAATGGAGAGAGCCTTAGATTCAGAGAGTGCCTATTTAGAAAACGAA 1380  
Db 1332 GAGCTAAGAGTAATGGAGAGAGCCTTAGATTCAGAGAGTGCCTATTTAGAAAACGAA 1391  
QY 1381 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAATPACCCCAACAGTACCAACATGAC 1440  
Db 1392 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGGAATPACCCCAACAGTACCTCAATGAC 1451  
QY 1441 ATGAAGGAATATTGGAAGCAGTTAGAGGAATPACCCCAACAGTACCTCAATGAC 1500  
Db 1452 ATGAAGGAATATTGGAAGCAGTTAGAGGAATPACCCCAACAGTACCTCAATGAC 1488

QY 1501 AAAACCTATTTTGGTGAAGAGAGTAACTTCCCTGTCTCCATCAAGATGCATCTGAGGGAGAA 1560  
Db 1489 ----- 1488  
QY 1561 GCACCTGTGACGACATTTGAAAAGACCTTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1620  
Db 1489 -----AGACATTTGAAAAGACCTTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1538  
QY 1621 AGTAAAAATCCAGAACAGAAATATAAAGCTAAAGAGGGGTAAAATTTGAAAATTAATTTA 1680  
Db 1539 AGTAAAAATCCAGAACAGAAATATAAAGCTAAAGAGGGGTAAAATTTGAAAATTAATTTA 1598  
QY 1681 GACAAATGTATTTCTGATGAAAACATCTCTCCAGAGGAAGAGGCAATGGATATACCAAT 1740  
Db 1599 GACAAATGTATTTCTGATGAAAACATCTCTCCAGAGGAAGAGGCAATGGATATACCAAT 1658  
QY 1741 GAAACCTTTGACCTTTGAGGATGCGCATGAAGTTTAAAGGAATATGAATGTCTAAAGGAGCAT 1800  
Db 1659 GAAACCTTTGACCTTTGAGGATGCGCATGAAGTTTAAAGGAATATGAATGTCTAAAGGAGCAT 1718  
QY 1801 GGAGATTATACAGACAAAGCATTTGAAAACTTCACTGCCAGAGAGCGGTTTTTCCAG 1860  
Db 1719 GGAGATTATACAGACAAAGCATTTGAAAACTTCACTGCCAGAGAGCGGTTTTTCCAG 1778  
QY 1861 CAGACT 1866  
Db 1779 CTGACT 1784

## RESULT 2

US-10-243-735-1

; Sequence 1, Application US/10243735

; Patent No. 6706510

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001212DIV

; CURRENT APPLICATION NUMBER: US/10/243,735

; CURRENT FILING DATE: 2002-09-16

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2370

; TYPE: DNA

; ORGANISM: Human

US-10-243-735-1

## Query Match

Best Local Similarity 80.6%; Score 1654; DB 4; Length 2370;

Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

QY 1 ATGGATAAGTAGATGTGATTAAGGCCATCGGGCAAGTGCCTTCGGGAAGCATCTT 60  
Db 12 ATGGATAAGTAGATGTGATTAAGGCCATCGGGCAAGTGCCTTCGGGAAGCATCTT 71  
QY 61 GCTAAAGGGAATTCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAAGATG 120  
Db 72 GCTAAAGGGAATTCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAAGATG 131  
QY 121 CCCATACAGAAAAAGAGCTTCAAGAAAGAGATGATCTTCTCGAAAAGATGAACAT 180  
Db 132 CCCATACAGAAAAAGAGCTTCAAGAAAGAGATGATCTTCTCGAAAAGATGAACAT 191  
QY 181 CCCAAGATTTGAGCTTCTTCAATTCATTTCAAGAGATGGCAGCTGTCTTATTTCTAATG 240  
Db 192 CCCAAGATTTGAGCTTCTTCAATTCATTTCAAGAGATGGCAGCTGTCTTATTTCTAATG 251  
QY 241 GAATATTTGATGGAGGGGATCTCATGAAAAGGATCAATAGAACACGGGGTGTGTTATTT 300  
Db 252 GAATATTTGATGGAGGGGATCTCATGAAAAGGATCAATAGAACACGGGGTGTGTTATTT 311

301 AGTGAAGATCAGATCCTCGTGGTGGTTGTACAGATTTCTAGGACTAAACATATTCAT 360  
Db AGTGAAGATCAGATCCTCGTGGTGGTTGTACAGATTTCTAGGACTAAACATATTCAT 371  
361 GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTCTTAGCAAGACGGA 420  
Db GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTCTTAGCAAGACGGA 431  
421 ATGGTGGCAAGCTTGGGACCTTTGGTATPAGAAGAGTCTCTGAATAATTCATGGAATC 480  
Db ATGGTGGCAAGCTTGGGACCTTTGGTATPAGAAGAGTCTCTGAATAATTCATGGAATC 491  
481 GCTCGAAGCTTGTATTGGACACCTTACTACCTGTCCTCCAGAGATCTGTCAGATTAACCC 540  
Db GCTCGAAGCTTGTATTGGACACCTTACTACCTGTCCTCCAGAGATCTGTCAGATTAACCC 551  
541 TACAACATAAAGCGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGACACAT 600  
Db TACAACATAAAGCGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGACACAT 611  
601 AACATCCTTTGAGGGTAACACTTACAGAGCTGGTTCTGAAGATTTGTCAAGCAGAT 660  
Db AACATCCTTTGAGGGTAACACTTACAGAGCTGGTTCTGAAGATTTGTCAAGCAGAT 671  
661 TTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
Db TTGCCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 731  
721 CAAGTATCTCTCGAGACGACATCCATAAATTCOAATTTGAAAGGCCCTTTTAGAG 780  
Db CAAGTATCTCTCGAGACGACATCCATAAATTCOAATTTGAAAGGCCCTTTTAGAG 791  
781 AATCTTATTTCCAAATATTGACTCTGAGGTCATTCAGGAGAAATTCAGTCACATGCTT 840  
Db AATCTTATTTCCAAATATTGACTCTGAGGTCATTCAGGAGAAATTCAGTCACATGCTT 851  
841 ATATGACAGAGCGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAAGTGTAA 900  
Db ATATGACAGAGCGAGCGCCAGCTTCTCGACATGCTGGGAAGTGGTCCAGAAAGTGTAA 911  
901 ATACAAAAGTGAGATTCAGGGAAGTCCCAACAGATCAAGATATCTGTGCCAAT 960  
Db ATACAAAAGTGAGATTCAGGGAAGTCCCAACAGATCAAGATATCTGTGCCAAT 971  
961 AAAAGGAATGCTATATTGCATAGAAATGAATGAGACACACAGCTGGAGCCCAAGGCC 1020  
Db AAAAGGAATGCTATATTGCATAGAAATGAATGAGACACACAGCTGGAGCCCAAGGCC 1031  
1021 AGATCTATAAATATAGAAAGCCAAATTTGCTGTGCTGTGAGCAATATGATAT 1080  
Db AGATCTATAAATATAGAAAGCCAAATTTGCTGTGCTGTGAGCAATATGATAT 1091  
1081 TATTATGCTCACTTGATATGCTGAGGAGAGGCCCAACACCAAGTTATCACCTATT 1140  
Db TATTATGCTCACTTGATATGCTGAGGAGAGGCCCAACACCAAGTTATCACCTATT 1151  
1141 CCTCAAGAAATATCTGGAGTTAGGATTAACGTCAGGAAACAGGAGCATGGTCCATCCCA 1200  
Db CCTCAAGAAATATCTGGAGTTAGGATTAACGTCAGGAAACAGGAGCATGGTCCATCCCA 1211  
1201 AGTCAATGGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAA 1260  
Db AGTCAATGGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAGTTGAA 1271  
1261 GTGGAAGCAATTTGGTCTTCTGCTCCATCTTCTGCGAGCCAAATTAACACAGAGCAA 1320  
Db GTGGAAGCAATTTGGTCTTCTGCTCCATCTTCTGCGAGCCAAATTAACACAGAGCAA 1331  
1321 GAGCTAAGAGTAATCGAGAGAGCCTAGATTCCAGAGCTGCCATTTAGGAAAAACGAA 1380  
Db GAGCTAAGAGTAATCGAGAGAGCCTAGATTCCAGAGCTGCCATTTAGGAAAAACGAA 1391

1381 ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGAAATATAGCCAAACAGTACCACATGAC 1440  
Db ATGAAGGAACAGGAATATTGGAAGCAGTTAGAGAAATATAGCCAAACAGTACCACATGAC 1451  
1441 ATGAAGGAATATTGGAAGGAATGCGGAGAGAAACCAAGAGGAGAACTCAAAAATAAGTCAT 1500  
Db ATGAAGGAATATTGGAAGGAATGCGGAGAGAAACCAAGAGGAGAACTCAAAAATAAGTCAT 1500  
1452 ATGAAGGAATATTGGAAGGAATGCGGAGAGAAACCAAGAGGAGAACTCAAAAATAAGTCAT 1488  
1501 AAAACCTATTGTTGGTGAAGAAGATTAACCTGCCTGCTCCATCAAGATGATCTGTAGGGAGAA 1560  
Db AAAACCTATTGTTGGTGAAGAAGATTAACCTGCCTGCTCCATCAAGATGATCTGTAGGGAGAA 1560  
1561 GCACCTGTGAGGACATTTGAAAAGAGCTTGAACAAATAGGCTTCCAGAACACAAAGGAA 1620  
Db GCACCTGTGAGGACATTTGAAAAGAGCTTGAACAAATAGGCTTCCAGAACACAAAGGAA 1620  
1489 AGGACATTTGAAAAGAGCTTGAACAAATAGGCTTCCAGAACACAAAGGAA 1538  
1621 AGTAAAATTCAGAACAGAAATATAAGCTAAGAGGGGGTAAATAATTTGAAAATTAATTTA 1680  
Db AGTAAAATTCAGAACAGAAATATAAGCTAAGAGGGGGTAAATAATTTGAAAATTAATTTA 1680  
1539 AGTAAAATTCAGAACAGAAATATAAGCTAAGAGGGGGTAAATAATTTGAAAATTAATTTA 1598  
1681 GACAAATGATTTCTGATGAACATCTCCAGAGGAAGGCAATGGATATATACCAAT 1740  
Db GACAAATGATTTCTGATGAACATCTCCAGAGGAAGGCAATGGATATATACCAAT 1740  
1599 GACAAATGATTTCTGATGAACATCTCCAGAGGAAGGCAATGGATATATACCAAT 1658  
1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAAGGAATATGAATGTGTAAGAGGAT 1800  
Db GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAAGGAATATGAATGTGTAAGAGGAT 1718  
1801 GGAGATTTATACAGAACAGATTTGAAAATCTTCACTGCCAGAGAGGAGGTTTCCACG 1860  
Db GGAGATTTATACAGAACAGATTTGAAAATCTTCACTGCCAGAGAGGAGGTTTCCACG 1860  
1719 GGAGATTTATACAGAACAGATTTGAAAATCTTCACTGCCAGAGAGGAGGTTTCCACG 1778  
1861 CAGACT 1866  
Db CTGACT 1784

## RESULT 3

US-09-620-312D-246  
; Sequence 246, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyun  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aiding J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pc\_files version 1.0  
; SEQ ID NO 246  
; LENGTH: 5448  
; TYPE: DNA



Db	1011	GCTCGA	ACTTGC	TAGGAC	CCCACT	ACTTGT	CACCTG	GAATCT	GTAACA	AAACCT	1070	
Qy	541	TACAACA	TAAACG	GATAT	TTTGGT	CTCTTG	GGTGTG	CTCTTA	TATAG	AGCTCT	GCACACTT	600
Db	1071	TACAATA	TAAAAA	GTGACA	TTGGCT	CTGGGG	TGTCTC	TTTAT	GAGCTG	TGTACACTT	1130	
Qy	601	AAACAT	CCCTTT	TGAGGT	TAAACA	CTTAC	GACAGC	TGCTT	CTGAAG	ATTTG	TCAAGCACAT	660
Db	1131	AAACAT	CCCTTT	TGAAGT	GTGCAG	TATG	AAAAA	CCGTCT	CGAAGA	TAAAT	CTGGATCT	1190
Qy	661	TTTGCC	CAATAT	CTCGGG	GTTTCT	CGTG	AGCTCC	ATTCC	TTTGAT	TATCT	CAGCTCTTT	720
Db	1191	TTTCC	ACCTGT	CTTTG	CATTAT	TTCCTA	TGATCT	CCG	CAGTTGG	TGTCT	CAGTATTT	1250
Qy	721	CAAGT	ATCTCT	CGAGAC	CGACAT	CAATAA	ATCCAT	TTTTG	AAAGGCC	CTTTT	TAGAG	780
Db	1251	AAAGA	AAATCCT	TAGGG	TAGACCA	TCACTC	CAACTC	CAATAT	TGGAGA	AAAGTTT	TATAGCC	1310
Qy	781	AACTCT	TATCCC	AAATAT	TTTGACT	CTCTG	AGGTCAT	TTCAG	GAAGAAT	TTCAGTC	832	
Db	1311	AAACG	CATTG	AAAAGT	TTCTCT	CTCC	TCAGCTT	ATTTC	GAGA	GAATTTT	TGTC	1362

## RESULT 5

US-09-166-350-29

; Sequence 29, Application US/09166350A

; Patent No. 6440663

**GENERAL INFORMATION:**

APPLICANT: Scanlan, Matthew

; APPLICANT: Chen, Yao

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Old, Lloyd

; APPLICANT: Jager, Elke

APPLICANT: Knuth, Alex

1. TITLE OF INVENTION: **Renal Cancer Associated Antigens and**

FILE REFERENCE: 10461/7051

FILE REFERENCE: L0461/7051  
CURRENT APPLICATION NUMBER: US/00/156 3503

; CURRENT APPLICATION NUMBER: US/09/166,350A  
 : CURRENT FILING DATE: 1998-10-05

CURRENT FILING DATE: 1998-10-05  
: EARLIER APPLICATION NUMBER: US 09/166,350

EARLIER FILING DATE: 1998-10-05

QUARTER FILING DATE: 1999-10-03  
NUMBER OF SEO ID NOS: 35

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 29

; LENGTH: 4263

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-166-350-29

Query Match 17.2%: Score 352: DB 4: Length 4263:

Best Local Similarity 64.8%; Pred. No. 5.4e-94;

Matches 539; Conservative 0; Mismatches 290; Indels 3; Gaps 1;

QY 1 ATGGATAAGTACGATGTGATTAAAGGCCATCGGGCAAGGTGCCCTTCGGGAAAGCATACTTA 60

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QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAATG 120

Db 636 GTTAAATCGACAGAGGATGCGAGACATTATGTTCATCAAGGAATTAAACATCTCAAGAA TG 695

---

[illegible]

Db 696 TCTGATAAAGAAAGGCAAGAAATCAAGGAGAGAAGTTGCTGTATTGGCAACATGAAGCAT 755

QY 181 CCCAACATTGTAGCCTTCTTCAATTCATTTCAAGAGAAATGGCAGGCTGTTTATTGTAATG 240



Query Match	11 68:	Score 238	4:	DB 3:	Length 1846:
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Query Match	11.66;
Best Local Similarity	67.58;

Best Local Similarity 97.3%, Freq: NO; 2:1E-007  
Matches 351: Conservative 0: Mismatches 166: Indels 3: Gaps 1:

313 ATCCTCGGTTGGTTGTACAGATTTCTCTAGGACTAAAAACATATTTCATTCACAGGAAGATA 372

QY JTS

373 TTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGACGGAATGGTGCAAG 432  
Db  
430 CTTATCGAGACATTAATCTCAGAACATATTTTAACTAAGATGGAACAGT---ACAA 486  
433 CTTGGGACTTTGGTATAGCAGAGCTCTGAATATTCATGGAACCTTGGCTGCAACTGT 492  
Db  
487 CTTGGAGATTTTGGAAATTCCTAGAGTCTTAATAGTACTGTAGAGCTGGCTCGAACTTC 546  
493 ATTGGAACACCTTACTACCTGTCCCGAGAGATCTCTCAGAAATAAACCCCTACAAATAAAA 552  
Db  
547 ATAGGACCCCATACTACTTGTACCTGAAATCTGTGAACACAACTTACAAATAAAA 606  
553 ACGGATATTGGTCTCTGGCTGTCTTATATAGCTCTGCACACTTAAACATCCTTTT 612  
Db  
607 AGTGACATTTGGGCTCTGGGCTGTCTCTTATAGCTGTGTACACTTAAACATGCTTTT 666  
613 GAGGCTAACAACTTACAGCAGCTGGTCTCTGAAGATTTGTCAAGACATTTTGGCCCAATA 672  
Db  
667 GAAGCTGGCAGTATGAACAACTGTACTGAGATAATATCTGGATCTTTTCCACCTGTG 726  
673 TCTCCGGGTTTCTCGTAGCTCCATTCCTTGTATATCTCAGCTCTTTCAGTATCTCT 732  
Db  
727 TCTTTGCATTTATCTCTATGATCTCCGAGTTTGGTGTCTCAGTTATTTAAAGAAATCT 786  
733 CGAGACCCGACCATCAATAATTCATTTTGAAGGCCCTTTTATAGAGAATCTTATCCC 792  
Db  
787 AGGATAGACCAATCAGTCACTCCATATTTGGAAGAGTTTATAGCCAAACGCAATTGAA 846  
793 AAATATTTGACTCTCGAGTCAATTCAGGAAGATTCAGTC 832  
Db  
847 AAGTTTCTCTCTCTCAGCTTATTCAGAGAATTTTGTG 886

## RESULT 7

US-09-420-915-15

; Sequence 15, Application US/09420915

; Patent No. 6264947

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Fang, Y. Tom

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Corley, Neil C.

; APPLICANT: Gorgone, Gina

; APPLICANT: Azimzai, Yalda

; APPLICANT: Lu, Aina

; TITLE OF INVENTION: Protein Kinase Homologs

; FILE REFERENCE: PF-0614 US

; CURRENT APPLICATION NUMBER: US/09/420,915

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/173,581

; EARLIER FILING DATE: 1998-10-15

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PERL Program

; SEQ ID NO 15

; LENGTH: 1846

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: 1567782

US-09-420-915-15

Query Match 11.6%; Score 238.4; DB 3; Length 1846;  
Best Local Similarity 67.5%; Pred. No. 2.1e-60;  
Matches 351; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

313 ATCCCTCGGTTGGTGTACAGATTTCTTAGGATTAACATATTCAGACAGGAATA 372  
Db  
370 ATTTTGGACTGGTTGTACAGATATGTTGGCCCTGGAACATGTACATGATAGAAAAT 429  
373 TTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGACGGAATGGTGCAAG 432

430 CTTATCGAGACATTAATCTCAGAACATATTTTAACTAAGATGGAACAGT---ACAA 486  
433 CTTGGGACTTTGGTATAGCAGAGCTCTGAATATTCATGGAACCTTGGCTGCAACTGT 492  
Db  
487 CTTGGAGATTTTGGAAATTCCTAGAGTCTTAATAGTACTGTAGAGCTGGCTCGAACTTC 546  
493 ATTGGAACACCTTACTACCTGTCCCGAGAGATCTCTCAGAAATAAACCCCTACAAATAAAA 552  
Db  
547 ATAGGACCCCATACTACTTGTACCTGAAATCTGTGAACACAACTTACAAATAAAA 606  
553 ACGGATATTGGTCTCTGGCTGTCTTATATAGCTCTGCACACTTAAACATCCTTTT 612  
Db  
607 AGTGACATTTGGGCTCTGGGCTGTCTCTTATAGCTGTGTACACTTAAACATGCTTTT 666  
613 GAGGCTAACAACTTACAGCAGCTGGTCTCTGAAGATTTGTCAAGACATTTTGGCCCAATA 672  
Db  
667 GAAGCTGGCAGTATGAACAACTGTACTGAGATAATATCTGGATCTTTTCCACCTGTG 726  
673 TCTCCGGGTTTCTCGTAGCTCCATTCCTTGTATATCTCAGCTCTTTCAGTATCTCT 732  
Db  
727 TCTTTGCATTTATCTCTATGATCTCCGAGTTTGGTGTCTCAGTTATTTAAAGAAATCT 786  
733 CGAGACCCGACCATCAATAATTCATTTTGAAGGCCCTTTTATAGAGAATCTTATCCC 792  
Db  
787 AGGATAGACCAATCAGTCACTCCATATTTGGAAGAGTTTATAGCCAAACGCAATTGAA 846  
793 AAATATTTGACTCTCGAGTCAATTCAGGAAGATTCAGTC 832  
Db  
847 AAGTTTCTCTCTCTCAGCTTATTCAGAGAATTTTGTG 886

## RESULT 8

US-09-873-404-3

; Sequence 3, Application US/09873404

; Patent No. 6500656

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Maxlon et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001212-CIP

; CURRENT APPLICATION NUMBER: US/09/873,404

; CURRENT FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 63588

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(63588)

; OTHER INFORMATION: n = A, T, C or G

US-09-873-404-3

Query Match 10.0%; Score 205.2; DB 4; Length 63588;  
Best Local Similarity 96.3%; Pred. No. 1.6e-49;  
Matches 210; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

606 TCTTTTGGAGGTAAACAATTTACAGCAGCTGGTCTCTGAAGATTTGTCAAGCAATTTTGC 665  
Db  
27430 TCAHTTTGAGGTACAACTTACAGCAGCTGGTCTCTGAAGATTTGTCAAGCAATTTTGC 27489  
666 CCAATATCTCCGGGTTTCTCGTAGCTCCATTCCTTGTATCTCAGCTCTTTCAAGT 725  
Db  
27490 CCAATATCTCCGGGTTTCTCGTAGCTCCATTCCTTGTATCTCAGCTCTTTCAAGT 27549  
726 ATCTCTCGAGACCCGACCATCAATAATTTCCATTTTGAAGGCCCTTTTATAGAGAACT 785  
Db  
27550 ATCTCTCGAGACCCGACCATCAATAATTTCCATTTTGAAGGCCCTTTTATAGAGAACT 27609  
786 TATTCCAAATATTTTACTCTCTCAGGTCATTCAGGAAG 823

Db 27610 TATTCCTCAATATTTGACCTCTGAGGTAAAGTTTGGG 27647

RESULT 9

US-10-243-735-3  
; Sequence 3, Application US/10243735  
; Patent No. 6706510  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001212DIV  
; CURRENT APPLICATION NUMBER: US/10/243,735  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 63588  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(63588)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-243-735-3

Query Match 10.0%; Score 205.2; DB 4; Length 63588;  
Best Local Similarity 96.3%; Pred. No. 1.6e-49;  
Matches 210; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 606 TCCTTTGAGGTAACTTACAGCAGCTGGTTCGAAGATTGTCAAGCATTGTC 665  
Db 27430 TCAGTTGAGGTAACTTACAGCAGCTGGTTCGAAGATTGTCAAGCATTGTC 27489  
QY 666 CCCAATATCTCCGGGTTTTCGTGAGCTCCATTCTTGATATCTCAGCTCTTTCAAGT 725  
Db 27490 CCCAATATCTCCGGGTTTTCGTGAGCTCCATTCTTGATATCTCAGCTCTTTCAAGT 27549  
QY 726 ATCTCTCGAGCCGACCATCCATAAATTCATTTTGAAGGCCCTTTTAGAGAACT 785  
Db 27550 ATCTCTCGAGCCGACCATCCATAAATTCATTTTGAAGGCCCTTTTAGAGAACT 27609  
QY 785 TATTCCTCAATATTTGACCTCTGAGGTCAATTCAGGAG 823  
Db 27610 TATTCCTCAATATTTGACCTCTGAGGTAAAGTTTGGG 27647

RESULT 10

US-09-992-481-1  
; Sequence 1, Application US/09992481  
; Patent No. 6593125  
; GENERAL INFORMATION:  
; APPLICANT: Friddle, Carl Johan  
; APPLICANT: Hilbun, Erin  
; APPLICANT: Mathur, Brian  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. 6593125el Human Kinases and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: LEX-0266-USA  
; CURRENT APPLICATION NUMBER: US/09/992,481  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/252,011  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2079  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-992-481-1

Query Match 8.3%; Score 170.2; DB 4; Length 2079;  
Best Local Similarity 52.1%; Pred. No. 4.5e-40;  
Matches 404; Conservative 0; Mismatches 368; Indels 3; Gaps 1;  
QY 1 ATGATAAGTACGATGTGATTAGGCCATCGGGCAAGTGCCTTCGGGAAAGCATACTTA 60  
Db 1 ATGGAGAAGTACGAGCGGATCCGAGTGGTGGGAGAGGTGCCTTCGGGATTGTGCACCTG 60  
QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAGATG 120  
Db 61 TGCCTGGGAAGGTGACAGAGCTGGTGTATCATCAAGCAGATTCCAGTGGAAACATG 120  
QY 121 CCCATAAAGAAAAGAGCTTCAAGAAAAGAGTGTATTTCTTGGAAAAAGATGAACAT 180  
Db 121 ACCAAGGAAGAGCGGAGGAGCCAGATGAGTGCAGAGTCTCTCAAGTGTCTCAACAC 180  
QY 181 CCCACATCTAGCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGTTTATGTATG 240  
Db 181 CCCAATGTGATTGAGTACTAGGAACTTCTCTGGAAGACAAAGCCCTTATGATCGCCATG 240  
QY 241 GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAAACGGGTGTGTTATTT 300  
Db 241 GAATATGACCAGCGGCACCTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCCTCTGCTG 300  
QY 301 AGTGAAGATCAGATCCTTCGGTGGTGTGATAGATTTCTCTAGGACTAAACATATTAT 360  
Db 301 GAGGAGGAGACCATCTCTGCACTTCTTCGTGCAGATCCTGCTGCATCATGTGCAC 360  
QY 361 GACAGGAAGATATTACACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420  
Db 361 ACCACCTCATCTCTGACCGAGACCTCAAGCCAGACATCTGCTTGAACACACCGC 420  
QY 421 ATGTGCGAAAGCTTGGGACTTTGGTATAGCAAGTCTCTGAATTAATTCATGGAACAT 480  
Db 421 ATGTGCTCAAGTCTGCTGATTTCCGCACTCTCCAAAGATCCT---TAGCAGCAAGCAAG 477  
QY 481 GCTCGAATCTGTATGTAAGACACACCTTACTACTGTCCTCCAGAGATCTCTCAGATAAACCC 540  
Db 478 GCCTACAGGTGGTGGTATCCCATGCTATATCTCCCTGAGCTGTGTAGGGCAAGCCC 537  
QY 541 TACAAACATAAAGCGATATTTGGTCTCTTGGTGTGTCTTATATGAGCTCTGCACACT 600  
Db 538 TACAAACAGAAAGTGTGATCTGGGCTGGCTGTCTCTACGAGCTGGCCAGCCTC 597  
QY 601 AACATCTTTTGGGTTAACTTACAGCAGTGGTCTCTGAAGATTGTCAAGCAGAT 660  
Db 598 AAGAGGCTTTCGAGGCTGCGAACTTCCAGCACTGGTGTCTGAAGATCATGAGTGGCACC 657  
QY 661 TTTGCCCCAATATCTCCGGGTTTCTCTGAGCTCCATTCTCTGATATCTCAGCTCTTT 720  
Db 658 TTTGCACTATCTCTGACCGGTACAGCCCTGAGCTTCCGAGCTGGTCTGAGTCTACTC 717  
QY 721 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGCCCTTTT 775  
Db 718 AGCCTGGAGCTTCCCGAGCGGCCACCACCTACGCACATCATGCGACAGGCCCTCT 772

RESULT 11

US-08-870-529-1  
; Sequence 1, Application US/08870529  
; Patent No. 6080557  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: IL-1/TNF- (ACTIVATED KINASE (ITAK),  
; TITLE OF INVENTION: AND METHODS OF MAKING AND USING THE SAME  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle



STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/870,529  
FILING DATE: 06-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2937  
US-08-870-529-1

Query Match 8.1%; Score 166.8; DB 3; Length 2940;  
Best Local Similarity 54.8%; Pred. No. 5.9e-39;  
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

QY 25 GCCATCGGCAAGTGCCTTCGGGAAGCATACCTTAGCTAAAGGGAATCATAGACAAG 84  
DB 169 GTCTGGCGCGGGCGCTTCGGGAAGCCAGCTGTACCGCCGCCAGGATGACTCA 228

QY 85 CACTCTGTCATAAAGAGATCAATTTTGAAGAAGATGAAACATCCCATACAGAAAGAGCTTCA 144  
DB 229 CTGGTTGTGTGGAAGAGATCAATTTTGAAGAAGATGAAACATCCCATACAGAAAGAGCTTCA 144

QY 145 AAGAAGAAGTGAATCTTCTGGAAGAAGATGAAACATCCCATACAGAAAGAGCTTCA 204  
DB 289 TTGAATGAGATAGTATTTCTGCACTGCTGCAAGCAGCAACATTTATGCTTACTACAT 348

QY 205 TCATTTCAAGAGATGGCAGGCTGTTTATTTGAATGGAATATTTGATGGAGGGAATCTC 264  
DB 349 CACTTCATGGAACAATACCAACGCTGCTGATTTGAGCTGGAATATTTGATGGAGGGAACCTG 408

QY 265 ATGAAAGGATCAATAGACACACGGGCTGTTTATTTAGTGAAGATCAGATCCTCGGTGG 324  
DB 409 TATGACAAATCTTCGTCAGAGGACAAGTTGTTTGAAGAGAGATGGTGTGTGTAC 468

QY 325 TTGTACAGATTTCTTAGGACTAAACATATTTATGAGAGATCAGATCCTCGGTGG 384  
DB 469 CTATTTCAAGATTTCTTAGGACTAAACATATTTATGAGAGATCAGATCCTCGGTGG 528

QY 385 ATAAAGCTCAGAACATTTTCTTAGCAGAGGGAATGTTGGCAAGCTTGGGACCTTT 444  
DB 529 ATAAAGCATTAATATTTTCTGACCAAG--GCNAACCTGATTAACCTTGGAGATTAT 585

QY 445 GGATAGCAAGAGTCTCGTAATTAATTTCCATGGAATTTGCTCGAATTTGATTTGGAACACT 504  
DB 586 GGCCTAGCAAGAACTTAAATTTCTGAGTATTTCCATGGCTGAGACGCTTGTGGGAACCTCA 645

QY 505 TACTACCTGCTCCAGAGATCTGTGAGATTAACCTTCAACATTAACCGGATTTGG 564  
DB 646 TATTACATGCTCCAGAGCTCTGTGAGAGTAAAGTACATTTCAAGTCTGATATCTGG 705

QY 565 TCTTTGGCTGTGCTTATATGAGCTCTGCACTTAAACATTCCTTTAGGGGTAAACAC 624  
DB 706 GCAGTTGGCTGCTCAATTTTGAATCTTAAAGAGGAGGCTTTGATGCTACAAAC 765

QY 625 TTACAGCAGCTGTTCTGAAGATTTGTCAAGCACAATTTTGC 666  
DB 766 CCACCTTAACCTGTGTGAAGATCGTCAAGGAATTCGGGCC 807

RESULT 12  
US-09-544-794-1  
Sequence 1, Application US/09544794  
Patent No. 6541232  
GENERAL INFORMATION:  
APPLICANT: Sims, John B.  
APPLICANT: Virga, G. Duke  
APPLICANT: Bird, Timothy A.  
TITLE OF INVENTION: Polypeptides Having Kinase Activity  
FILE REFERENCE: 2005-B  
CURRENT APPLICATION NUMBER: US/09/544,794  
CURRENT FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 08/870,529  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/059,979  
PRIOR FILING DATE: 1996-06-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2940  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2940)  
US-09-544-794-1

Query Match 8.1%; Score 166.8; DB 4; Length 2940;  
Best Local Similarity 54.8%; Pred. No. 5.9e-39;  
Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

QY 25 GCCATCGGCAAGTGCCTTCGGGAAGCATACCTTAGCTAAAGGGAATCATAGACAAG 84  
DB 169 GTCTGGCGCGGGCGCTTCGGGAAGCCAGCTGTACCGCCGCCAGGATGACTCA 228

QY 85 CACTCTGTCATAAAGAGATCAATTTTGAAGAAGATGAAACATCCCATACAGAAAGAGCTTCA 144  
DB 229 CTGGTTGTGTGGAAGAGATCAATTTTGAAGAAGATGAAACATCCCATACAGAAAGAGCTTCA 288

QY 145 AAGAAGAAGTGAATCTTCTGGAAGAAGATGAAACATCCCATACAGAAAGAGCTTCA 204  
DB 289 TTGAATGAGATAGTATTTCTGCACTGCTGCAAGCAGCAACATTTATGCTTACTACAT 348

QY 205 TCATTTCAAGAGATGGCAGGCTGTTTATTTGAATGGAATATTTGATGGAGGGAATCTC 264  
DB 349 CACTTCATGGAACAATACCAACGCTGCTGATTTGAGCTGGAATATTTGATGGAGGGAACCTG 408

QY 265 ATGAAAGGATCAATAGACACACGGGCTGTTTATTTAGTGAAGATCAGATCCTCGGTGG 324  
DB 409 TATGACAAATCTTCGTCAGAGGACAAGTTGTTTGAAGAGAGATGGTGTGTGTAC 468

QY 325 TTGTACAGATTTCTTAGGACTAAACATATTTATGAGAGATCAGATCCTCGGTGG 384  
DB 469 CTATTTCAAGATTTCTTAGGACTAAACATATTTATGAGAGATCAGATCCTCGGTGG 528

QY 385 ATAAAGCTCAGAACATTTTCTTAGCAGAGGGAATGTTGGCAAGCTTGGGACCTTT 444  
DB 529 ATAAAGCATTAATATTTTCTGACCAAG--GCNAACCTGATTAACCTTGGAGATTAT 585

QY 445 GGATAGCAAGAGTCTCGTAATTAATTTCCATGGAATTTGCTCGAATTTGATTTGGAACACT 504  
DB 586 GGCCTAGCAAGAACTTAAATTTCTGAGTATTTCCATGGCTGAGACGCTTGTGGGAACCTCA 645

QY 505 TACTACCTGCTCCAGAGATCTGTGAGATTAACCTTCAACATTAACCGGATTTGG 564  
DB 646 TATTACATGCTCCAGAGCTCTGTGAGAGTAAAGTACATTTCAAGTCTGATATCTGG 705

QY 565 TCTTTGGCTGTGCTTATATAGAGCTCTGCACACTTAAACATCCTTTTGGAGGTAACAAC 624  
 Db |||||  
 706 GCAGTTGGCTGGCTCATTTTGAAGCTTACCTTAAGAGGACGCTTTGATGCTACAAAC 765  
 QY 625 TTACAGCAGCTGGTCTGAAGATTGTGTAAGACACATTTTGGC 666  
 Db |||||  
 766 CCACTTAACCTGTGTGAAGATCGTGAAGGATTCGGGCC 807

## RESULT 13

US-08-870-529-8  
 ; Sequence 8, Application US/08870529  
 ; Patent No. 6080557  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sims, John E.  
 ; APPLICANT: Virca, G. Duke  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Anderson, Dirk M.  
 ; TITLE OF INVENTION: IL-1/TNF- $\alpha$ -ACTIVATED KINASE (ITAK),  
 ; TITLE OF INVENTION: AND METHODS OF MAKING AND USING THE SAME  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/870,529  
 ; FILING DATE: 06-JUN-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mcmasters, David D.  
 ; REGISTRATION NUMBER: 33,963  
 ; REFERENCE/DOCKET NUMBER: 480052.418  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3264 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

US-08-870-529-8  
 Query Match 8.1%; Score 166.8; DB 3; Length 3264;  
 Best Local Similarity 54.8%; Pred. No. 6.3e-39;  
 Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

QY 25 GCATCGGCAAGGTCCTTCGGAAAGCATCTTAGCTAAAGGAAATCAGATAGCAAG 84  
 Db |||||  
 288 GTCTCGGCGCGGCGCTTCGGGAGGACGCTGTACCGCGCGCACCGAGATGACTCA 347  
 QY 85 CACTGTGTCAATAAAGAGATCAATTTTGAAGAAGATGCCCATACAGAAAAAGAGCTTCA 144  
 Db |||||  
 348 CTGGTTGTGTGAAGGAAGTCGATTGTACCCGGCTGTCTGAGAAGGAAGCTGTGATGCC 407  
 QY 145 AAGAAGAGTGTATCTTCTGGAAGATGAACATCCCAACATTTGAGCCTTCTTCAAT 204  
 Db |||||  
 408 TTGAATGAGATGATTTATCTGGCACTGCTGCGAGCAGCAACATTTATGCTTACTACAT 467  
 QY 205 TCATTTCAGAGAAATGCGAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTC 264  
 Db |||||  
 468 CACTTCATGACAATACCACCGCTGCTGATTGAGCTGGAATATTGTAATGAGGGAACCTG 527

QY 265 ATGAAAAGGATCAATAGACAACCGGGTGTGTTATTATTAGTGAAGATCAGATCCTCGGTGG 324  
 Db |||||  
 528 TATGACAAATCCTTCGTGAGAGGACAAGTTGTTTGAGGAAGAGATGGTGTGCTGCTAC 587  
 QY 325 TTGTACAGATTTCTTAGGACTTAAACATATTTCATGACAGGAAGATATTACACAGGAC 384  
 Db |||||  
 588 CTATTTAGATTTGTTTCAGCAGTGAGCTGCATCCATAAGCTGGAATCCTTTCATAGAGAT 647  
 QY 385 ATAAAAGCTCAGAACATTTTCTTAGCAAGAAAGGAATGTTGGCAAAAGCTTTGGGGACTTT 444  
 Db |||||  
 648 ATAAAGACATTAATAATTTTCTGACCAAG--GCAAACTGATAAACTTGGAGATTAT 704  
 QY 445 GGTATAGCAAGAGCTCTGAATAATTCCATGGAATTCCTCGAATTCCTGTAATTTGNAACCT 504  
 Db |||||  
 705 GGCCTAGCAAGAAACTTAAATTTCTGAGTATTTCCATGCTCAGACGCTTGTGGGAACCCCA 764  
 QY 505 TACTACCTGTCCTCCAGAGATCTGTGAGATAAAACCCCTACAACTAAACCGGATATTGG 564  
 Db |||||  
 765 TATTACATGCTCCAGAGCTCTGTCAAGGAGTAAGTACATTTCAAGTCTGATATCTGG 824  
 QY 565 TCTCTTGGCTGTGCTTATATGAGCTCTGCACACTTAAACATCTTTTGGAGGTAAACAAC 624  
 Db |||||  
 825 GCAGTTGGCTGGCTCATTTTGAACCTGTTACCTTAAAGAGGACGTTTGTGCTACAAAC 884  
 QY 625 TTACAGCAGCTGTTCTGAAGATTGTCAAGCACATTTTGGC 666  
 Db |||||  
 885 CCACTTAACCTGTGTGAAGATCGTCAAGGAATTCGGGCC 926

## RESULT 14

US-09-544-794-8  
 ; Sequence 8, Application US/09544794  
 ; Patent No. 6541232  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sims, John E.  
 ; APPLICANT: Virca, G. Duke  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Anderson, Dirk M.  
 ; TITLE OF INVENTION: Polypeptides Having Kinase Activity  
 ; FILE REFERENCE: 2005-B  
 ; CURRENT APPLICATION NUMBER: US/09/544,794  
 ; CURRENT FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: 08/870,529  
 ; PRIOR FILING DATE: 1997-06-06  
 ; PRIOR APPLICATION NUMBER: 60/059,979  
 ; PRIOR FILING DATE: 1996-06-10  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 3264  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-09-544-794-8  
 Query Match 8.1%; Score 166.8; DB 4; Length 3264;  
 Best Local Similarity 54.8%; Pred. No. 6.3e-39;  
 Matches 352; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

QY 25 GCCATCGGCAAGGTCCTTCGGAAAGCATCTTAGCTAAAGGAAATCAGATAGCAAG 84  
 Db |||||  
 288 GTCTCGGCGCGGCGCTTCGGGAGGACGCTGTACCGCGCACCGAGATGACTCA 347  
 QY 85 CACTGTGTCAATAAAGAGATCAATTTTGAAGAAGATGCCCATACAGAAAAAGAGCTTCA 144  
 Db |||||  
 348 CTGGTTGTGTGAAGGAAGTCGATTGTACCCGGCTGTCTGAGAAGGAACGTCGTGATGCC 407  
 QY 145 AAGAAGAGTGTATCTTCTGGAAGATGAACATCCCAACATTTGAGCCTTCTTCAAT 204  
 Db |||||  
 408 TTGAATGAGATGATTTATCTGGCACTGCTGAGCAGCAACATTTATGCTTACTACAT 467  
 QY 205 TCATTTCAGAGAAATGCGAGGCTGTTTATTGTAATGGAATATTGTGATGGAGGGATCTC 264  
 Db |||||  
 468 CACTTCATGACAATACCACGCTGCTGATTGAGCTGGAATATTGTAATGAGGGAACCTG 527

QY 265 ATCAAAAGGATCAATAGACAAAGCGGTGTGTTATTAGTGAAGATCAGATCCTCGGTGG 324  
 Db 528 TATGACAAATCCTTCGTCAGAAGGACAAAGTTGTTTGGAGAGAGATGGTGTGTGTAC 587  
 QY 325 TTTGTACAGATTCTCTAGGACTAAACAATATTCATGACAGAGATATTAACACAGGAC 384  
 Db 588 CTATTTCAGATTGTTTCAGCAGTGTGCTGCATCCATAAGCTGGAATCCTTCATAGAT 647  
 QY 385 ATAAAGCTCAGAACATTTTCTTAGCAAGACGAATGGTGGCAAGCTTGGGACTTT 444  
 Db 648 ATAAAGCATTAATATTTTCTGACCAAG---GCAACCTGTATTAACCTTGGAGATTAT 704  
 QY 445 GGTATAGCAAGAGTCTCTGAATTAATTCATGGAACCTTGTGCAACCTTGTATGGAACCT 504  
 Db 705 GGCCTAGCAAGAACTTAATCTGAGTATTCATGCTGAGACGCTTGTGGGAACCCCA 764  
 QY 505 TACTACCTGTCCAGAGATCTGTGAGATTAACCTTACCAATTAACCGGATATTGG 564  
 Db 765 TATTACATGCTCCAGAGCTGTGCAAGAGTAAAGTAAATTTCAAGTCTGATATCTGG 824  
 QY 565 TCTCTGGGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTGGGGTAAACAAC 624  
 Db 825 GCAGTTGGCTGGTCAATTTTGAACCTGTACCTTAAAGAGGAGCTTTGATGCTACAAC 884  
 QY 625 TTACAGCAGCTGGTCTGAAGATTGTCAAGCAATTTTGGC 566  
 Db 885 CCACCTTAACCTGTGTGAAGATCTGCAAGGAATTCGGGCC 926

RESULT 15

US-10-196-927-3  
 ; Sequence 3, Application US/10196927  
 ; Patent No. 6797510  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Friddle, Carl Johan  
 ; TITLE OF INVENTION: No. 6797510el Human Kinases and Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0348-USA  
 ; CURRENT APPLICATION NUMBER: US/10/196,927  
 ; CURRENT FILING DATE: 2002-05-20  
 ; PRIOR APPLICATION NUMBER: US 60/293,248  
 ; PRIOR FILING DATE: 2001-05-24  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1449  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-196-927-3

Query Match 6.4%; Score 131.6; DB 4; Length 1449;  
 Best Local Similarity 51.3%; Pred.No. 1.1e-28;  
 Matches 364; Conservative 0; Mismatches 334; Indels 12; Gaps 2;  
 QY 91 GTCATAAAAGAGATCAATTTTGAAGAAGTGCCTACAGAAAAAGAGCTTCAAGAAA 150  
 Db 175 GTACTTAAGGAAATATCTGTTGGAGAACTAAATCCAAATGAACTGTACAGGCCAATTG 234  
 QY 151 GAAGTGATTTCTGGAAAAGATGAACATCCCACTGTAGCCTTCTCAATTCATTT 210  
 Db 235 GAAGCCCAACTCCTTCCAACTGGACCCCAAGCCATTTGCAAGTTCCATGCAAGTTT 294  
 QY 211 CAAGAGATGGCAGGCTGTTTATGTAATGGAATATTGTGATGGAGGGATCTCATGAAA 270  
 Db 295 GTGGAGCAAGATAATTTCTGCATTATACGAGTACTGTGAGGCCGAGATCTGACGAT 354  
 QY 271 AGGATCA-----ATAGACACGGGGTGTGTTATTAGTGAAGATCAGATCCTCGGTGG 324  
 Db 355 AAAATTCAGGAATATAACAGCTGGAATAATCTTCCAGAAAAATCAAAATTAAGATGG 414  
 QY 325 TTTGTACAGATTCTCTAGGACTAAACATATTTCATGACAGGAAGATATTACACAGGAC 384

Db 415 TTTATCCAGCTGCTGTGGAGTTGACTACATGATGAGAGGAGATACCTTCATCGAGAC 474  
 QY 385 ATAAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGGTGGCAAGCTTGGGACTTT 444  
 Db 475 TTAAGTCAAGAGATGATTTCTGAAAATAA-----TCTCTTAATTTGAGATTTT 528  
 QY 445 GGTATAGCAAGAGTCTCTGAATTAATTCATGGAACCTTGTGCAACCTTGTATGGAACA 504  
 Db 529 GGAGTTTCTCGACTTCTAATGGATCCTGTGACCTGGCCACAACTTTAACTGGAACCTCC 588  
 QY 505 TACTACCTGTCCAGAGATCTGTGAGATTAACCTTACCAATTAACCGGATATTGG 564  
 Db 589 CATTAATGAGTCTGAGGCTCTGAAACACCAAGGCTATGACACAAAGTCGGACATCTGG 648  
 QY 565 TCTCTTGGGTGTCTTATATGAGCTCTGCACACTTAAACATCCTTTTGGGGTAAACAAC 624  
 Db 649 TCACTGGCATGCATTTTGTATGAGATGCTGTGATGATCATGCTGCTGCTCCAAT 708  
 QY 625 TTACAGCAGCTGGTCTGAGATTTGTCAAGCAATTTTGGCCCAATATCTCGGGGTTT 684  
 Db 709 TTTTATCCATTTGTTTAAAAATTTGTTGAAGGTGACACACCTTCTCTCCCTGAGAGAT 768  
 QY 685 TCTCGTGAGCTCCATTCCTTTGATATCTCAGCTCTTTCAAGTATCTCCTCGAGACCGACA 744  
 Db 769 CAAAAGAACTAAATGCCATCATGGAAGCATGTTGAACAAGATCCCTTCATTAGACCA 828  
 QY 745 TCCATAAATTCATTTTGAAGAGGCTTTTGAAGAGATCTTTTAGAGATCTTTATCCCAA 794  
 Db 829 TCTGCTATCGAAATTTTAAAAATCCCTTACCTTTGATGAGCAGCTACAGAA 878

Search completed: October 10, 2004, 08:49:42  
 Job time : 234 secs

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		Match	%				
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	2	843.8	41.1	890	5	BX350584	BX350584
	3	814.6	39.7	980	5	EX342707	EX342707 BX342707
	4	595.4	29.0	1434	3	AK054168	AK054168 Mus muscu
	5	595.4	29.0	2407	3	AK032672	AK032672 Mus muscu
	6	594	28.9	603	9	AY405588	AY405588 Homo sapi
	7	576.4	28.1	872	5	BX417448	BX417448 Homo sapi
	8	536.8	26.2	670	6	CD700193	CD700193 EST16717
	9	514.8	25.1	928	5	BQ917635	BQ917635 AGENCOURT
	10	474	23.1	856	6	CD343608	CD343608 AGENCOURT
11	464.8	22.7	603	9	AY405589	AY405589 Pan trogl	
12	455.4	22.2	603	9	AY405590	AY405590 Mus muscu	
13	452.4	22.0	659	2	BX666328	BX666328	
14	447.8	21.8	678	5	BX328262	BX328262 BX328262	
15	390	19.0	639	2	B8623078	B8623078	
16	389.6	19.0	643	2	B8665975	B8665975 B8665975	
17	368	17.9	1628	3	BC015147	BC015147 Homo sapi	
18	361.6	17.6	857	7	CN158710	CN158710 947521 MA	
19	352	17.2	2070	3	AK031330	AK031330 Mus muscu	
20	352	17.2	5362	3	BC070443	BC070443 Mus muscu	
21	350.4	17.1	3568	3	AK077047	AK077047 Mus muscu	
22	343.2	16.7	3103	3	AK034754	AK034754 Mus muscu	
23	328.4	16.0	648	4	B0061491	B0061491 BJ061491	
24	320.2	15.6	904	5	BX369829	BX369829 BX369829	



Db 711 TTGGGACTTTTGTATAGCAAGAGTCTCTGAATAATTCATGGAACCTTGTCTGCACTTGTGA 552

Qy 494 TTGGACACCTTACTACTCTGTCCTCCAGAGATCTGTGAGATAAAACCTTCAACAATAAAA 553

Db 651 TTGGACACCTTACTACTCTGTCCTCCAGAGATCTGTGAGATAAAACCTTCAACAATAAAA 592

Qy 554 CGGATATTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGACACATTAACATTCCTTTTG 613

Db 591 CGGATATTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGACACATTAACATTCCTTTTG 532

Qy 614 AGGTTAACTTACAGAGCTGGTCTGAAGATTTGTCAAGCACATTTTGGCCCCAATAT 673

Db 531 AGGTTAACTTACAGAGCTGGTCTGAAGATTTGTCAAGCACATTTTGGCCCCAATAT 472

Qy 674 CTCGGGGTTTCTCTGAGCTCCATTCCTTGATATCTCAGCTCTTCAAGTATCTCCTC 733

Db 471 CTCGGGGTTTCTCTGAGCTCCATTCCTTGATATCTCAGCTCTTCAAGTATCTCCTC 412

Qy 734 GAGACCGACCATCAATAATTCATTTTGAAGAGGCCCTTTTATAGAAATCTTATTCOCA 793

Db 411 GAGACCGACCATCAATAATTCATTTTGAAGAGGCCCTTTTATAGAAATCTTATTCOCA 352

Qy 794 ATATTTGACTCTGAGGTCATTCAGAGAAATTCAGTCACATGCTTATATGCAAGGAG 853

Db 351 ATATTTGACTCTGAGGTCATTCAGAGAAATTCAGTCACATGCTTATATGCAAGGAG 292

Qy 854 GAGCGCCAGCTTCTGCACATCTCTGGGAAGTGTCCAGAAAGTGTAAATACAAAAAGTGA 913

Db 291 GAGCGCCAGCTTCTGCACATCTCTGGGAAGTGTCCAGAAAGTGTAAATACAAAAAGTGA 232

Qy 914 GATTCAGGAAAGTCCCAACAAATCAAGATATCTGTGCAATTAAGGAATGCTA 973

Db 231 GATTCAGGAAAGTCCCAACAAATCAAGATATCTGTGCAATTAAGGAATGCTA 172

Qy 974 TATTGCATGAATGAATGGAGACCAACAGCTGGAGCCAGAGCCAGATCTATAAAA 1033

Db 171 TATTGCATGAATGAATGGAGACCAACAGCTGGAGCCAGAGCCAGATCTATAAAA 112

Qy 1034 TGATAGAAAGACCAAAATTTGCTGTCTGTGGACATATGATTATTTATGCTCAAC 1093

Db 111 TGATAGAAAGACCAAAATTTGCTGTCTGTGGACATATGATTATTTATGCTCAAC 52

Qy 1094 TTGATATGCTGGAGGAGAGCCCAACCAAGTTATCACCCATTTC 1141

Db 51 TTGATATGCT-AGGAGGAGAGCCCAACCAAGTTATCACCCATTTC 5

## RESULT 3

LOCUS BX342707 980 bp mRNA linear EST 08-APR-2004

DEFINITION Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED

ACCESSION BX342707

VERSION BX342707.2 GI:46279550

KEYWORDS EST.

## SOURCE

Homosapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 980)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30344086.

## COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dN) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster

6942.r.

and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see <http://www.genoscope.cns.fr/cdna?s=CS0DL005BF09QPI&c=6942.r>.

## FEATURES

## source

1..980

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clones="CS0DL005YK18"

/cell\_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/cell\_line="RAMOS CELL LINE"

/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dN) primer. Five prime end enriched, double-strand cDNA was digested with NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 39.7%; Score 814.6; DB 5; Length 980;

Best Local Similarity 97.7%; Pred. No. 1.4e-196;

Matches 863; Conservative 5; Mismatches 9; Indels 6; Gaps 4;

Qy 1 ATGGATAGTACGATGTGATTAAAG-GCCATCGGCAAGGTGCTTCGGGAAAGCATACTT 59

Db 94 ATGGATAGTACGATGTGATTAAAGCCCATCGGCAAGGTGCTTCGGGAAAGCATACTT 153

Qy 60 AGCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTGAAAAGAT 119

Db 154 AGCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTGAAAAGAT 213

Qy 120 GCCCATCAAGAAAAGAGGCTTCAAGAAAGAGTGTCTTCTGAAAAGATGAAACA 179

Db 214 GCCCATCAAGAAAAGAGGCTTCAAGAAAGAGTGTCTTCTGAAAAGATGAAACA 273

Qy 180 TCCCAACATTTAGCTTCTTCAATTCAATTCAGAGATGGCAGGCTGTATTATGTAAT 239

Db 274 TCCCAACATTTAGCTTCTTCAATTCAATTCAGAGATGGCAGGCTGTATTATGTAAT 333

Qy 240 GGAATATTGTGATGGAGGATCTCATGAAAGGATCAATAGACACGGGCTGTATTAT 299

Db 334 GGAATATTGTGATGGAGGATCTCATGAAAGGATCAATAGACACGGGCTGTATTAT 393

Qy 300 TAGTGAAGATCAGATCCTCGTGGTTTGTACAGATTTCTTAGGACTAAACATATTC 359

Db 394 TAGTGAAGATCAGATCCTCGTGGTTTGTACAGATTTCTTAGGACTAAACATATTC 453

Qy 360 TGACAGAGATATTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGAAGCG 419

Db 454 TGACAGAGATATTACACAGGACATATAAGCTCAGAACATTTTCTTAGCAAGAAGCG 513

Qy 420 AATGGTGGCAAGCTTGGGACCTTGGTATAGCAAGAGTCTCTGAATAATTTCCATGGA 479

Db 514 AATGGTGGCAAGCTTGGGACCTTGGTATAGCAAGAGTCTCTGAATAATTTCCATGGA 573

Qy 480 TGCTCGAATTTGATTTGGAACACCTTACTACCTGTGCTCCAGAGATCTGTGAGATAAAC 539

Db 574 TGCTCGAATTTGATTTGGAACACCTTACTACCTGTGCTCCAGAGATCTGTGAGATAAAC 633

Qy 540 CTACAACAATAAAACGATATTGGTCTCTTGGCTGTCTTATATAGAGCTCTGCACACT 599

Db 634 CTACAACAATAAAACGATATTGGTCTCTTGGCTGTCTTATATAGAGCTCTGCACACT 693

Qy 600 TAAACATCTTTTGAAGGTTAAACATTTACAGAGCTGGTTCTGAAGATTTGTCAAGACA 659

Db 694 TAAACATCTTTTGAAGGTTAAACATTTACAGAGCTGGTTCTGAAGATTTGTCAAGACA 752

Qy 660 TTTTGGCCCAATATCTCCGGGTTTCTCTGCTGAGCTCCATTCCTTGATATCTCAGCTCT 719

Db 753 TTTTGGCCCAATATCTCCGGGTTTCTCTGCTGAGCTCCATTCCTTGATATCTCAGCTCT 812

Qy 720 TCAAGTATCTCCTCGAGACCGACCATCCATAAATTCATTTTGAAAAAGGCCCTTTTAG 779

Db 813 TCAGTATCTCTCCGAGACCGACCATCATTAATTCATTTTGAAGGCCCTTTTAGA 872  
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 Db 873 GAATCTTATTCCTCAATATTTGACTCTGAGGTGATTCAGGAGAAATTCATGTCATGCT 931  
 Qy 840 TATATGCGAGAGAGCGGCGAGCTTCTCGACATGCTCGGAG 882  
 Db 932 TATATGCGAG--AGAGGAGCGCACTTCTCGACATGCTCGRAG 971

RESULT 4  
 AK054168  
 LOCUS  
 DEFINITION Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230024112 product:weakly similar to protein kinase nek1 (EC 2.7.1.-) [Mus musculus], full insert sequence.  
 ACCESSION AK054168  
 VERSION 1 GI:26344040  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Katsunai, T., Tashiro, H., Itoh, M., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurikawa, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, N., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
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Db      361  TTATATGAGCTGTGCACACTTAAACATCTTTTGGGGTAAACAATTACAGCAGCTGGTT 420
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Qy      700  TCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCAT 759
Db      481  TCTTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAAATTCAT 540
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Db      601  GA 602

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DEFINITION
BX417448 5-PRIME, mRNA sequence.
ACCESSION
BX417448
VERSION
BX417448.2 GI:46926799
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
On May 13, 2003 this sequence version replaced gi:30642067.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6942.r
There is a virtual cDNA representing this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cdnas?CS0DE009CE04QPI&C=6942.r.
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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## FEATURES

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1..872
/organism="Homo sapiens"
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with a NotI-oligo(dT) primer. Five prime end enriched,
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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

Query Match 28.1%; Score 576.4; DB 5; Length 872;
Best Local Similarity 84.3%; Pred. No. 9.2e-136;
Matches 696; Conservative 1; Mismatches 122; Indels 7; Gaps 4;

ORIGIN
CD700193 human nasopharynx Homo sapiens cDNA, mRNA sequence.
EST16717 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD700193
VERSION CD700193.1 GI:32230189
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 670)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)

```

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Qy      204  TTCTATTCAAGAGATGGCAGCTGTGTTTATTGTAATGGAATATTGTGATGAGGGGATCT 263
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Db      827  AGAATGAATGGAGA-CMCCAGCTGGAGCCCAAGGAGATCTATA 871

```

COMMENT

Contact: Vixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 DongFeng Road East, GuangZhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@zsus.edu.cn

FEATURES

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LOCUS  
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5', mRNA sequence.  
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VERSION BQ917635.1 GI:22332333  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 928)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE

JOURNAL

COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Susan L. Sullivan, PhD.  
cDNA Library Preparation: ResGen, Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13735 row: i column: 18  
High quality sequence stop: 734.

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Library."

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QY 640 CTGAAGATTGTCAAGACATTTTGGCCCAATATCTCGGGGTTTCTCTGAGCTCCAT 699  
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QY 760 TTGAAAGGCCCTTTTAGAGAACTTATCCCAATATTGACTCTCGAGTCAATCAG 819  
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 Db 601 GA 602

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 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 603)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 603)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
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 Db 61 AGGACGCGGGAGTGATGTTTCAGCGAAGACAGATCCCTGTTGTTGTTGTACAGATTCT 120

QY 340 CTAGGACTAAACATATTCTACGAGGAGATATTACACGGGACATTAAGGCTCAGAAC 399  
 Db 121 CTAGGACTAAACATATTCTACGAGGAGATATTACACGGGACATTAAGGCTCAGAAC 180

QY 400 ATTTTCTTTAGCAAGACGGAATGTCGAACTTGTATTGGAACACCTTACTCTGCCCA 459  
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QY 460 CTGAATAATTTCCATGGAATCTGCTGAACTTGTATTGGAACACCTTACTCTGCCCA 519  
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QY 520 GAGATCTGTGACAAATGTCGAACTTGTATTGGAACACCTTACTCTGCCCA 579  
 Db 301 GAGATCTGTGACAAATGTCGAACTTGTATTGGAACACCTTACTCTGCCCA 360

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QY 640 CTGAAGATTGTCAAGACATTTTGGCCCAATATCTCGGGGTTTCTCTGAGCTCCAT 699  
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QY 760 TTGAAAGGCCCTTTTAGAGAACTTATCCCAATATTGACTCTCGAGTCAATCAG 819  
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 Db 601 G 601

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 VERSION BB666328.1 GI:16499961  
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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 659)

## REFERENCE AUTHORS

1 (bases 1 to 659)  
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T.,  
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
 Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
 Onno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, S.,  
 Sugabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
 Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ENKs (Arakawa, T., et al. 2001)

TITLE	JOURNAL	COMMENT

Query Match	22.0%;	Score 452.4;	DB 2;	Length 659;
Best Local Similarity	84.8;	Pred. No. 4e-104;		
Matches 507;	Conservative 0;	Mismatches 91;	Indels 0;	Gaps 0
Qy	213	AGAAATGGCAGGCTGTTATTATGTAATGGAATATTGTGATCGAGGGGATCTCATGAAAG	272	
Db	53	AGAAACGGCAGGCTGTTATTGTAATGGAATACTGTGATGGAGGGATCTCATGCAGAG	112	
Qy	273	GATCAATAGACACGGGGTGTGTTATTGCTGAAGATCAGATCCTCGGTGGTTGTGACA	332	
Db	113	GATCCAGAGCGGGGAGTGATGTTTCGCGAAGACGAGATCCTGTGTGGTTGTGACA	172	
Qy	333	GATTTCTTAGGACTAAACATATTATGACGAGGAATATTACAGGGGACATAAAAGC	392	
Db	173	GATTTCTTAGGACTGAAGCATATTTCATGACGAGGAATTTTACAGGGGACATAAAATC	232	
Qy	393	TCGAAACATATTTCTTTAGCAAGACGGAATGGTGGCAAGCTTCGGGACATTTGGTATAGC	452	
Db	233	TCGAATATATTTCTTTAGCAAGATGAATGGTGTGCCAAGCTCGGGAGATTTGGAAACGC	292	
Qy	453	AAGAGTCTGAATTAATTCATGGAACCTTGCTCGAACCTTGTTTGGAAACACCTTACTACCT	512	
Db	293	AAGAAACACTGAATGACATCCATGGAACTTGCTCAACATGTGCTCGGACACCTTACTACCT	352	
Qy	513	GTCCCCAGAGATCTGTGAGAAATAAACCCCTACAAACAATAAAACGGATATTTGGTCTCTTGG	572	
Db	353	GTCCCCAGAGATCTGTGAGAACAGCCCATACAAACAATAAACGGACATCTGGTCTCTTGG	412	
Qy	573	CTGTGCTTTATATGAGCTCTGACACATTAACATCTCTTTTGGGGTTAACAACTTACAGCA	632	
Db	413	CTGTGCTTTATATGAGCTCTGACACATCAAGCATCTCTTTTGGAGAGCAACAACTTCCACCA	472	
Qy	633	GCTGGTTCTGAAGATTTGTCAAGCACATTTTGGCCCCAATATCTCCGGGGGTTTCTCGTGA	692	
Db	473	TCTGGTTCTGAAGATTTGTCAAGAGCGTGTGTCTCCCATATCATCCCCACTTCTCTCGTGA	532	
Qy	693	GCTCCATCTCTGATATCTCAGCTCTTCAAGTATCTCTCGAGACCGACCATCCATAA	752	
Db	533	CCATAGTCTCTGATACCTCAGCTCTTTCAGAGTGTCTCTTCAGAGCCGGGCATCCGTTAC	592	
Qy	753	TTCCATTTTCAAAAGGCCCTTTTTCAGAGAACTTTATTTCCCAAAATATTTCAGTCTCTGAG	810	
Db	593	GTCCCTTTTCAAAAGACCTTTTTCAGAAATCTCATTTGCCGATCTCTTTGTATCTGAG	650	

source

RESULT	14
Locus	BX328262
LOCUS	
DEFINITION	BX328262 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED EST 08-APR-2004
ACCSSION	BX328262
VERSION	BX328262.2 GI:46281552 linear mRNA
KEYWORDS	Homo sapiens cDNA clone CSODL005VK18 5-PRIME, mRNA sequence.
SOURCE	EST.
DATABASE	Homo sapiens (human)
ORGANISM	Homo sapiens
TAXID	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CENTROID	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PARENT	1 (bases 1 to 678)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalized
JOURNAL	Unpublished (2001)
COMMENT	On May 2, 2003 this sequence version replaced gi:30344693.

mouse brain, cerebellum, and testis. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken. Divided to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGCGGCGCAACTGAGTGTGTGTGTGTGTGTN 3'], cDNA was prepared by using trehalase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATTCTCGATTATTAATAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

## ORIGIN







Best Local Similarity 82.7%; Pred. No. 3.4e-88;  
Matches 463; Conservative 0; Mismatches 85; Indels 12; Gaps 1;

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QY 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGGTGCCTTCGGGAAGCATACTTA 60
Db |||||
QY 92 ATGGATAACTTTACCTGATTAAAGATCATGGGAAGGCACCTTTGGGAAGGTGACTTG 151
Db |||||
QY 61 GCTAAAGGGAATCAGATAGCAGCAGCTGTGCATAAAAGAGATCAATTTTGAAGAAGTG 120
Db |||||
QY 152 GCTAAAGATAAATCAGAAAGCAGTCAGTGTGCATAAAAGAAATCAGTTTGACAAAG--- 208
Db |||||
QY 121 CCCATACAGAAAGAAAGAGCTTCAAGAAAGAGAGTGAATCTTCTGGAAGAGTGAACAT 180
Db |||||
QY 209 -----GAAAAAGAGCCCTCAAGAAACGAAAGTGAATCTTCTGGCTAGGATGGAGCAT 259
Db |||||
QY 181 CCCAAGATTGTAGCCTTCTCAATTCTTCAATTCAAGAGAAATGGCAGGCTGTTTATTGTAATG 240
Db |||||
QY 260 CCCAATATCGTAACCTTCTTCAGCTCGTTTCAAGAGACGGCAGGCTGTTTATTGTAATG 319
Db |||||
QY 241 GAATATTGTGATGGAGGGGATCTCATGAAAGGATCAATAGACAAACGGGGTGTGTTATT 300
Db |||||
QY 320 GAATATCTGTGATGGAGGGGATCTCATGAGAGGATCCAGAGGACGGGGAGTGATGTTTC 379
Db |||||
QY 301 AGTGAAGATCAGATCCTCGTTGGTTTGTACAGATTTCTTAGGACTAAACATATTTCAT 360
Db |||||
QY 380 ASCGAGACCCAGATCCTGTGTGGTTTGTACAGATTTCTTAGGACTGAAGCATATTTCAT 439
Db |||||
QY 361 GACAGGAAGATATTACAGGGACACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
Db |||||
QY 440 GACAGGAAGATTTTACAGGGACACATAAAATCTCAGATATTTTCTTAGCAAGAAATGGA 499
Db |||||
QY 421 ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGTCCCTGAATAATTCATGGAATTT 480
Db |||||
QY 500 ATGGTTGCCAAGCTCGGGACCTTTGGAACAGCAAGAACACTGAATGACTCCATGGAATTT 559
Db |||||
QY 481 GCTCGAATTTGATTGGAAACACTTACTACTCTGTCCTCCAGAGATCTGTGAGAATAAAACC 540
Db |||||
QY 560 GCTCAACATGTGCTGGGACCTTTACTACTCTGTCCTCCAAAGATCTGGCAGAACAGGCCA 619
Db |||||
QY 541 TACAACATATAAACGGATAT 560
Db |||||
QY 620 TACAACAATAAAACGGACAT 639
Db |||||
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Search completed: October 10, 2004, 11:30:09  
Job time : 9621 secs



GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 22:26:00 ; Search time 1426 Seconds  
(without alignments)  
7553.865 Million cell updates/sec

Title: US-09-940-921B-1

Perfect score: 2052  
Sequence: 1 atggataagtcagatgtgat.....cagtgctcatcctgatgtga 2052

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq 23Sep04: \*  
1: Geneseqn1980s: \*  
2: Geneseqn1990s: \*  
3: Geneseqn2000s: \*  
4: Geneseqn2001as: \*  
5: Geneseqn2001bs: \*  
6: Geneseqn2002as: \*  
7: Geneseqn2002bs: \*  
8: Geneseqn2003as: \*  
9: Geneseqn2003bs: \*  
10: Geneseqn2003cs: \*  
11: Geneseqn2003ds: \*  
12: Geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2052	100.0	2052	6	Abk12424 cDNA enco
2	2052	100.0	2240	6	Abk12426 Novel hum
3	1976.4	96.3	2816	12	Adj96571 Human Nim
4	1868	91.0	1965	6	Abk12425 cDNA enco
5	1654	80.6	2370	8	Abk12425 cDNA enco
6	1469.6	71.6	1947	4	Aas06745 Polynucle
7	1359.8	66.3	1896	8	Abz59716 Human NEK
8	1359.8	66.3	1918	8	Abz59717 Human NEK
9	1190.2	58.0	1587	8	Abx72263 Human NOV
10	1178.4	57.4	1453	8	Abx72262 Human NOV
11	602	29.3	1632	10	Abz77151 Human pro
12	595.4	29.0	1434	10	Adf44502 Mouse kin
13	595.4	29.0	2407	10	Adf44489 Mouse kin
14	368	17.9	3645	5	Aas11558 Human cDN
15	368	17.9	3729	8	Aal51590 Human ser
16	368	17.9	4683	8	Abx13160 Human cDN
17	368	17.9	5426	5	Aas11582 Human cDN
18	368	17.9	5448	4	Aal58367 Human pol
19	368	17.9	5448	5	Adg98576 DNA enco
20	368	17.9	5448	9	Abd48336 Novel hum
21	368	17.9	5508	8	Aal51591 Human ser

22	368	17.9	5532	4	Aai58366 Human pol
23	368	17.9	5532	5	Adg98575 DNA enco
24	368	17.9	5532	9	Adb48335 Novel hum
25	368	17.9	5583	12	Adj96572 Human Nim
26	360	17.5	5514	4	Aai60152 Human pol
27	360	17.5	5514	4	Aai60153 Human pol
28	358.8	17.5	2343	6	Abv75946 Ser/Thr/T
29	352	17.2	4263	3	Aaa09328 Human can
30	260.8	12.7	1588	8	Abx72261 Human NOV
31	260.8	12.7	1588	12	Adh42550 Novel hum
32	259.2	12.6	1781	8	Abx72260 Human NOV
33	259.2	12.6	1781	12	Adh42548 Novel hum
34	259.2	12.6	2257	8	Abx72259 Human NOV
35	259.2	12.6	2257	12	Adh42546 Novel hum
36	253.8	12.4	876	4	Aah06097 Human cDN
37	253.8	12.4	2975	4	Aah17731 Human cDN
38	253.8	12.4	2975	8	Aal51593 Human ser
39	253.2	12.3	1578	8	Abz68773 Nucleotid
40	252.8	12.3	1581	8	Abz68735 Nucleotid
41	252.8	12.3	1991	12	Adi40889 Human kin
42	252.8	12.3	2050	10	Acc99119 Human KPP
43	252.8	12.3	2102	6	Abz69800 Human ser
44	252.8	12.3	2110	6	Aad38850 Human kin
45	252.8	12.3	2220	4	Aak51477 Human pol

## ALIGNMENTS

RESULT 1  
ABK12424  
ID ABK12424 standard; cDNA; 2052 BP.  
XX  
AC ABK12424;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE cDNA encoding novel human kinase protein #1.  
XX  
KW Novel human protein; NHP; serine-threonine kinase; brain;  
KW calcium/calmodulin-dependent kinase; myosin light chain kinase;  
KW biological disorder; spleen; placenta; chromosome 6; gene; ss.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..2052  
FT /\*tag= a  
FT /product= "Human kinase protein #1"  
XX  
FN WO200218555-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 28-AUG-2001; 2001WO-US026776.  
XX  
PR 31-AUG-2000; 2000US-0229280P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Friddle CJ, Hilbun E, Nepomnichy B, Hu Y;  
XX  
DR WPI; 2002-292200/33.  
XX  
DR P-PSDB; AAU77928.  
XX  
PT Novel polynucleotide encoding novel human protein sharing structural  
PT similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-  
PT dependent, and myosin light chain kinases, useful as probes and primers.  
XX  
PS Claim 1; Page 37-38; 46pp; English.  
XX  
CC The present invention relates to the isolation of novel human proteins  
(NHPs) and the polynucleotide sequences encoding them. The NHPs of the

CC invention are kinase proteins and share structural similarity to serine-  
 CC threonine, calcium/calmodulin-dependent, and myosin light chain kinases.  
 CC The sequences of the invention are useful for treating biological  
 CC disorders. The polynucleotide sequences encoding the kinase proteins can  
 CC be used as primers and probes. The sequences are also useful for  
 CC identifying mutations associated with a particular disease and also in a  
 CC prognostic or diagnostic assay. The present sequence encodes human  
 CC protein kinase #1 which is expressed in a broad range of human tissues  
 CC such as brain, spleen, and placenta. The gene encoding protein kinase #1  
 CC is located on chromosome 6  
 XX

SQ Sequence 2052 BP; 698 A; 388 C; 482 G; 484 T; 0 U; 0 Other;

Query Match 100.0%; Score 2052; DB 6; Length 2052;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGTAAGTACGATCTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	60
DB	1	ATGGTAAGTACGATCTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	60
QY	61	GCTAAGGGAATCAGATAGCAAGCACTGTCTCAATAAAGAGATCAATTTTGAAGAAGT	120
DB	61	GCTAAGGGAATCAGATAGCAAGCACTGTCTCAATAAAGAGATCAATTTTGAAGAAGT	120
QY	121	CCCATACAAAGAAAGAGCTTCAAGAAAGAGTATCTTCGGAAGAGATGAACAT	180
DB	121	CCCATACAAAGAAAGAGCTTCAAGAAAGAGTATCTTCGGAAGAGATGAACAT	180
QY	181	CCCAACATTTAGCTCTCTCAATTCATTTCAAGAGAGTGCAGCTGTATTGTAATG	240
DB	181	CCCAACATTTAGCTCTCTCAATTCATTTCAAGAGAGTGCAGCTGTATTGTAATG	240
QY	241	GAATATTGTATGGAGGGGATCTCATGAAAGAGTCAATAGACAACGGGGTGTATT	300
DB	241	GAATATTGTATGGAGGGGATCTCATGAAAGAGTCAATAGACAACGGGGTGTATT	300
QY	301	AGTGAAGATCAGATCCTCGGTGGTGTGTACAGATTTCTTAGACATAAACATATTCAT	360
DB	301	AGTGAAGATCAGATCCTCGGTGGTGTGTACAGATTTCTTAGACATAAACATATTCAT	360
QY	361	GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA	420
DB	361	GACAGGAAGATATTACAGAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA	420
QY	421	ATGGTGGCAAGCTTGGGGAATTTGGTATAGCAAGTCCCTGAATATTCATGGAACCTT	480
DB	421	ATGGTGGCAAGCTTGGGGAATTTGGTATAGCAAGTCCCTGAATATTCATGGAACCTT	480
QY	481	GCTCGAATCTGTATTGGAAACCTTACTACTCTGCTCCAGAGATCTGTGAGAATAAACCC	540
DB	481	GCTCGAATCTGTATTGGAAACCTTACTACTCTGCTCCAGAGATCTGTGAGAATAAACCC	540
QY	541	TACAAACAATAACCGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT	600
DB	541	TACAAACAATAACCGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT	600
QY	601	AAACATCTTTTGGAGGTAAACAATTCAGAGCTGTGTTCTGAAGATTTGTCAAGACAT	660
DB	601	AAACATCTTTTGGAGGTAAACAATTCAGAGCTGTGTTCTGAAGATTTGTCAAGACAT	660
QY	661	TTTGCCCAATATCTCCGGGTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTT	720
DB	661	TTTGCCCAATATCTCCGGGTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTT	720
QY	721	CAAGTATCTCTCGAGCGGACCATCAATAATTCATTTTGAAGGCGCTTTTATAG	780
DB	721	CAAGTATCTCTCGAGCGGACCATCAATAATTCATTTTGAAGGCGCTTTTATAG	780
QY	781	AATCTTATTTCCAAATATTTGACTCTCTGAGTCAATTCAGGAGAAATTCAGTCAATGCTT	840
DB	781	AATCTTATTTCCAAATATTTGACTCTCTGAGTCAATTCAGGAGAAATTCAGTCAATGCTT	840

QY	841	ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGAAAGTGGTCCAGAAAGTGTAAA	900
DB	841	ATATGCAGAGCAGGAGCGCCAGCTTCTCGACATGCTGGAAAGTGGTCCAGAAAGTGTAAA	900
QY	901	ATACAAAAGTGAATTCAGGGAAGTCCCAACAGATCAAGGATATCTGTGCAATT	960
DB	901	ATACAAAAGTGAATTCAGGGAAGTCCCAACAGATCAAGGATATCTGTGCAATT	960
QY	961	AAAAGGAATGCTATATTGATAGAAATGAATGGAGACCAACAGCTGGAGCCAGAGGCC	1020
DB	961	AAAAGGAATGCTATATTGATAGAAATGAATGGAGACCAACAGCTGGAGCCAGAGGCC	1020
QY	1021	AGATCTATATAAATGATAGAAAGACCCAAAATTTGCTGTCTGTGGACATATGATAT	1080
DB	1021	AGATCTATATAAATGATAGAAAGACCCAAAATTTGCTGTCTGTGGACATATGATAT	1080
QY	1081	TATTATGCTCAACTTGAATGCTGAGGAGGAGCCCAACCAAGTATATCACCTTAT	1140
DB	1081	TATTATGCTCAACTTGAATGCTGAGGAGGAGCCCAACCAAGTATATCACCTTAT	1140
QY	1141	CCTCAAGAAAATTAATCGGATTCAGGATTAACGGTCAAGAAAACGAGCATGGTCCAT	1200
DB	1141	CCTCAAGAAAATTAATCGGATTCAGGATTAACGGTCAAGAAAACGAGCATGGTCCAT	1200
QY	1201	AGTCAATGSCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAA	1260
DB	1201	AGTCAATGSCCTGCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAA	1260
QY	1261	GTGGAAGCAATTTGGTCTTCTGCTCCATTTCTGCGAGCCAAATTAACAACAGAGCAA	1320
DB	1261	GTGGAAGCAATTTGGTCTTCTGCTCCATTTCTGCGAGCCAAATTAACAACAGAGCAA	1320
QY	1321	GAGCTAAGAAATTAAGGAGAGGCTAGATTCAGAGGAGCTGCCATTTAGGAAAACGAA	1380
DB	1321	GAGCTAAGAAATTAAGGAGAGGCTAGATTCAGAGGAGCTGCCATTTAGGAAAACGAA	1380
QY	1381	ATGAAGGAACAGAAATTTGGAGAGCAGTTAGAGGAATAACGCCAACAGTACCACATGAC	1440
DB	1381	ATGAAGGAACAGAAATTTGGAGAGCAGTTAGAGGAATAACGCCAACAGTACCACATGAC	1440
QY	1441	ATGAAGAAATTTAGAAAGAGTGGGAGAGAACCCAGAGGAGAACTCAAAATTAAGTCA	1500
DB	1441	ATGAAGAAATTTAGAAAGAGTGGGAGAGAACCCAGAGGAGAACTCAAAATTAAGTCA	1500
QY	1501	AAAACTATTTCGTGAAGAGAGTAACCTGCTGCTCCATCAAGATGCTCTGAGGAGAA	1560
DB	1501	AAAACTATTTCGTGAAGAGAGTAACCTGCTGCTCCATCAAGATGCTCTGAGGAGAA	1560
QY	1561	GCACTGTGCGAGCAATTTGAAAAGAGCTTGAACAAATAGGCTTCAGAACACAAAGGAA	1620
DB	1561	GCACTGTGCGAGCAATTTGAAAAGAGCTTGAACAAATAGGCTTCAGAACACAAAGGAA	1620
QY	1621	AGTAAATTCAGAACAGAAATATAAGCTAAGAGGGGTAAATTTGAAATTAATTA	1680
DB	1621	AGTAAATTCAGAACAGAAATATAAGCTAAGAGGGGTAAATTTGAAATTAATTA	1680
QY	1681	GACAAATGTAATTTCTGATGAAAACATCTCTCAAGAGGAGGCAATGGATATACAAAT	1740
DB	1681	GACAAATGTAATTTCTGATGAAAACATCTCTCAAGAGGAGGCAATGGATATACAAAT	1740
QY	1741	GAAATCTTCACTTTGAGGATGCGATGAATTTAGGATATGAATGTGTAAGAGGAT	1800
DB	1741	GAAATCTTCACTTTGAGGATGCGATGAATTTAGGATATGAATGTGTAAGAGGAT	1800
QY	1801	GGAGATTATACAGACAAAGCAATTTGAAAACCTTCACTGCCAGAGAGCAGGGTTTTCCACG	1860
DB	1801	GGAGATTATACAGACAAAGCAATTTGAAAACCTTCACTGCCAGAGAGCAGGGTTTTCCACG	1860
QY	1861	CAGACTGTAGTCTGTGGGAAACAGGAGGAGTGGGATGGAGGAGCGCTCAGACTCTG	1920
DB	1861	CAGACTGTAGTCTGTGGGAAACAGGAGGAGTGGGATGGAGGAGCGCTCAGACTCTG	1920
QY	1921	CTGCAGATGATGCGAGTGGCGGCATCACCTCCACTGCCCCCAGGGGCTTCAGAGTGAG	1980

Db 1921 CTGCAGATGATGGCAGTGGCCGACATCACCTCGCCACCGGGCCTGACAGTGAG 1980  
Qy 1981 TCTGTCTTAGCTCAGTGGTCAAGGAGGAGACCAAGGACCCGTACAGCCCGAGTGCTC 2040  
Db 1981 TCTGTCTTAGCTCAGTGGTCAAGGAGGAGACCAAGGACCCGTACAGCCCGAGTGCTC 2040  
Qy 2041 ATCCTGATGGA 2052  
Db 2041 ATCCTGATGGA 2052

RESULT 2  
ABK12426  
ID ABK12426 standard; cDNA; 2240 BP.

XX AC ABK12426;  
XX 18-JUN-2002 (first entry)  
DE Novel human protein ORF and flanking cDNA sequence #1.  
XX  
XX Novel human protein; NHP; serine-threonine kinase;  
KW calcium/calmodulin-dependent kinase; myosin light chain kinase;  
XX biological disorder; gene; ss.  
XX  
OS Homo.sapiens.

XX WO200218555-A2.  
XX 07-MAR-2002.  
XX 28-AUG-2001; 2001WO-US026776.  
XX 31-AUG-2000; 2000US-0229280P.  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX Fiddle CJ, Hilbun E, Nepomnichy B, Hu Y;  
XX WPI; 2002-292200/33.  
XX

PT Novel polynucleotide encoding novel human protein sharing structural  
PT similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-  
PT dependent, and myosin light chain kinases, useful as probes and primers.  
XX  
XX Disclosure; Page 42; 46pp; English.

XX The present invention relates to the isolation of novel human proteins  
CC (NHPs) and the polynucleotide sequences encoding them. The NHPs of the  
CC invention are kinase proteins and share structural similarity to serine-  
CC threonine, calcium/calmodulin-dependent, and myosin light chain kinases.  
CC The sequences of the invention are useful for treating biological  
CC disorders. The polynucleotide sequences encoding the kinase proteins can  
CC be used as primers and probes. The sequences are also useful for  
CC identifying mutations associated with a particular disease and also in a  
CC prognostic or diagnostic assay. The present sequence represents NHP ORF  
CC (open reading frame) and flanking cDNA sequence #1

XX Sequence 2240 BP; 749 A; 430 C; 515 G; 546 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 2052; DB 6; Length 2240;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATAAGTACGATGTGATTAGGCCATCGGCAAGGTGCTCGGGAAGCATACTTTA 60  
Db 105 ATGGATAAGTACGATGTGATTAGGCCATCGGCAAGGTGCTCGGGAAGCATACTTTA 164  
Qy 61 GCTTAAAGGGAATTCAGATGACGACACTGTGTCTATATAAAGAGATCAATTTTGAAGAATG 120  
Db 165 GCTTAAAGGGAATTCAGATGACGACACTGTGTCTATATAAAGAGATCAATTTTGAAGAATG 224

Qy 121 CCCATACAAGAAAGAGCTTCAAGAAAGAGTGAATCTTCTTGGAAAAAGATGAACAT 180  
Db CCCATACAAGAAAGAGCTTCAAGAAAGAGTGAATCTTCTTGGAAAAAGATGAACAT 284  
Qy 181 CCCAACATCTGAGCTTCTTCAATTCATTTCCAGAGATGGCAGGCTGTTTATGTATG 240  
Db CCCAACATCTGAGCTTCTTCAATTCATTTCCAGAGATGGCAGGCTGTTTATGTATG 344  
Qy 241 GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAAACCGGGTGTATTT 300  
Db GAATATTGTGATGAGGGGATCTCATGAAAAGGATCAATAGACAAACCGGGTGTATTT 404  
Qy 301 AGTGAAGATCAGATCCCTGGTGGTGTGATCAGAGTTTCTTAGGACTTAAACATATT 360  
Db AGTGAAGATCAGATCCCTGGTGGTGTGATCAGAGTTTCTTAGGACTTAAACATATT 464  
Qy 361 GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTTCTTAGCAAGACGGA 420  
Db GACAGGAAGATATTACACAGGGACATAAAAGCTCAGAACATTTTTCTTAGCAAGACGGA 524  
Qy 421 ATGTGGCAAGCTTGGGGACTTTGGTATAGCAAGAGTCTGTAATAATTCCATGGAATCT 480  
Db ATGTGGCAAGCTTGGGGACTTTGGTATAGCAAGAGTCTGTAATAATTCCATGGAATCT 584  
Qy 481 GCTCGAACTTGTATTGGAAACACCTTACTCTGCTCCAGAGATCTGTCAAGATAAACCC 540  
Db GCTCGAACTTGTATTGGAAACACCTTACTCTGCTCCAGAGATCTGTCAAGATAAACCC 644  
Qy 541 TACAACAATAAACCGGATATTGGTCTCTTGGTGTGCTTATATAGCTCTGCACACTT 600  
Db TACAACAATAAACCGGATATTGGTCTCTTGGTGTGCTTATATAGCTCTGCACACTT 704  
Qy 601 AAACATCTTTTGGGGTACAACTTACAGCAGCTGGTCTGAGATTTCGACAGACAT 660  
Db AAACATCTTTTGGGGTACAACTTACAGCAGCTGGTCTGAGATTTCGACAGACAT 764  
Qy 661 TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGTATATCTCAGCTCTT 720  
Db TTTGCCCCAATATCTCCGGGGTTTTCTCGTGAGCTCCATTCCTTGTATATCTCAGCTCTT 824  
Qy 721 CAAGTATCTCTCGAGACCGACCATCCATAAATCCATTTTGAAGGCCCTTTTAGAG 780  
Db CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGCCCTTTTAGAG 884  
Qy 781 AATCTTTATCCCAATATTGACCTCTGAGTCAATCAGGAAGAAATTCAGTCAATGCTT 840  
Db AATCTTTATCCCAATATTGACCTCTGAGTCAATCAGGAAGAAATTCAGTCAATGCTT 944  
Qy 841 ATATGACAGACAGGCGCCAGCTTCTCGACATGCTGGGAAGGTGTCGAGAAATGTAAA 900  
Db ATATGACAGACAGGCGCCAGCTTCTCGACATGCTGGGAAGGTGTCGAGAAATGTAAA 1004  
Qy 901 ATACAAAAGTGAGATTCAGGGAAGTGGCCCAAGATCAAGGATATCTGTGCCAATT 960  
Db ATACAAAAGTGAGATTCAGGGAAGTGGCCCAAGATCAAGGATATCTGTGCCAATT 1064  
Qy 961 AAAAGGAATGCTATATTGTCATAGAAATGAATGGAGACCAACAGCTGGAGCCCAAGGCC 1020  
Db AAAAGGAATGCTATATTGTCATAGAAATGAATGGAGACCAACAGCTGGAGCCCAAGGCC 1124  
Qy 1021 AGATCTATAAATGATAGAAAGCCCAAAATTCCTGCTGCTGTGACATATGATAT 1080  
Db AGATCTATAAATGATAGAAAGCCCAAAATTCCTGCTGCTGTGACATATGATAT 1184  
Qy 1081 TATTATGCTCAACTTGTATGCTGAGGAGGAGGCCCAAAATTCACCTTAT 1140  
Db TATTATGCTCAACTTGTATGCTGAGGAGGAGGCCCAAAATTCACCTTAT 1244  
Qy 1141 CCTCAAGAAATATCTGAGTTGAGGATTCGGTCAGGAAACGAGGATGTGTCCATCCCA 1200  
Db CCTCAAGAAATATCTGAGTTGAGGATTCGGTCAGGAAACGAGGATGTGTCCATCCCA 1304  
Qy 1201 AGTCAATGGCTGCTGAGTACCTTTCAGAGAAAAATTTTGAAGCTCAACAATATAGTTGAAA 1260

Db	1305	AGTCAAATGGCGCTCTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAAATATAAGTTGAAA	1364
Qy	1261	GTGGAGAAGCAATTTGGTCTTTCGTCCATCTTCTGCCAGGCAAAATTACAAACCAGAGACAA	1320
Db	1365	GTGGAGAAGCAATTTGGTCTTTCGTCCATCTTCTGCCAGGCAAAATPACACCCAGAGACAA	1424
Qy	1321	GAGCTAAGAAGTAATGGAGAAGAGCCTAGAATTCACAGAGCTGCCATTTTAGAAAAACGAA	1380
Db	1425	GAGCTAAGAAGTAATGGAGAAGAGCCTAGAATTCAGAGAGTGCATTTAGAAAAACGAA	1484
Qy	1381	ATGAAGAAACAGAAATATTGGAAGCAGTTAGAGGAAATAGCCAAACAGTACCACAAATGAC	1440
Db	1485	ATGAAGAAACAGAAATATTGGAAGCAGTTAGAGGAAATACGCCAACAGTACCACAAATGAC	1544
Qy	1441	ATGAAGAAATTTAGAAGAAGATGGGAGAGAACCCAGAGAGAACTCAAAAAATAAGTCAT	1500
Db	1545	ATGAAGAAATTTAGAAGAAGATGGGAGAGAACCCAGAGAGAACTCAAAAAATAAGTCAT	1604
Qy	1501	AAAACTTATTGTGTGAAGAAGAGTAACCTCCCTGTCCATCAAGATGCATCTGAGGGAGAA	1560
Db	1605	AAAACTTATTGTGTGAAGAAGAGTAACCTCCCTGTCCATCAAGATGCATCTGAGGGAGAA	1664
Qy	1561	GCACTGTGCAGACATTTGAAAAGACTTGAAACAAATGAGGCTTGAGAACACAAAGGAA	1620
Db	1665	GCACTGTGCAGACATTTGAAAAGACTTGAAACAAATGAGGCTTGAGAACACAAAGGAA	1724
Qy	1621	AGTAAAAATCCAGAACAGAAATATAAGCTTAAGAGGGGGTAAAAATTGAAATTAATTTA	1680
Db	1725	AGTAAAAATCCAGAACAGAAATATAAGCTTAAGAGGGGGTAAAAATTGAAATTAATTTA	1784
Qy	1681	GACAAATGTAATTTCTGATGAAAAATCCTCCAGAGAGGAAGAGGCAATGGATATACCAAT	1740
Db	1785	GACAAATGTAATTTCTGATGAAAAATCCTCCAGAGAGGAAGAGGCAATGGATATACCAAT	1844
Qy	1741	GAAACTTTGACCTTTGAGGATGCAATGAAGTTTAAAGGAATATGAATGTGTAAGAGGAGCAT	1800
Db	1845	GAAACTTTGACCTTTGAGGATGCAATGAAGTTTAAAGGAATATGAATGTGTAAGAGGAGCAT	1904
Qy	1801	GGAGATATACAGACAAAGCATTTGAAAAACTTCACTGCCAGAGAGAGGGTTTTCCACG	1860
Db	1905	GGAGATATACAGACAAAGCATTTGAAAAACTTCACTGCCAGAGAGAGGGTTTTCCACG	1964
Qy	1861	CACACTGACTCTGTGGGAAACAGAGAGCAGTGGGATGGAGAGCGCCTCAGACTCTG	1920
Db	1965	CACACTGACTCTGTGGGAAACAGAGAGCAGTGGGATGGAGAGCGCCTCAGACTCTG	2024
Qy	1921	CTCAGATGATGCAGTGGCCGACATCACTCCACTGCCCCACGGGGCTGACAGTGAG	1980
Db	2025	CTCAGATGATGCAGTGGCCGACATCACTCCACTGCCCCACGGGGCTGACAGTGAG	2084
Qy	1981	TCGTGCTTAGCTCAGTCTGAGGAGGGAAGCAAGGACCCGTACAGCCAGTGCTC	2040
Db	2085	TCGTGCTTAGCTCAGTCTGAGGAGGGAAGCAAGGACCCGTACAGCCAGTGCTC	2144
Qy	2041	ATCCTGATGTGA	2052
Db	2145	ATCCTGATGTGA	2156

### RESULT 3

ADJ96571

ID ADJ96571 standard; DNA; 2816 BP.

XXXX

AC ADJ96571;



DT 06-MAY-2004 (first entry)

XX  
XX

DE Human Nim-A related protein kinase NEK5 DNA SeqID 28.

[illegible]

KW gene; ds; kinase; human; tyrosine protein kinase;  
KW serine/threonine protein kinase: PTK. STK. gene therapy: cancer.

KW	neuronal associated disease; metabolic; inflammatory disorder;
KW	cytostatic; neuroprotective; immunomodulator; antiinflammatory;
KW	Nim-A related protein kinase; NEX5.
XX	
XX	
OS	Homo sapiens.
OS	52.
XX	
PN	WO2004006838-A2.
XX	
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PD	22-JAN-2004.
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PF	15-JUL-2003; 2003WO-US021730.
XX	
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PR	15-JUL-2002; 2002US-0395632P.
XX	
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PA	(SUG-) SUGEN INC.
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PI	Whyte D, Manning G, Caenepeel S;
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DR	WPI; 2004-122753/12.
DR	P-PSDB; ADJ96637.
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XX	
PT	New nucleic acid molecule encoding a kinase polypeptide, useful for
PT	preparing a composition for treating diseases or disorders, e.g., cancer,
PT	or neurological, immunological or inflammatory disorders.

Query Match	96.3%;	Score 1976.4;	DB 12;	Length 2816;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1977: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

678 GACAGGAAGATATTACAGAGGACATAAAAGCTCAGAACATTTTCTTAGCAAGACGGA 737  
 421 ATGGTGGCAAGCTTGGGACATTTGGTATAGCAAGAGTCTCCTCAATAATTCATGGAATC 480  
 738 ATGGTGGCAAGCTTGGGACATTTGGTATAGCAAGAGTCTCCTCAATAATTCATGGAATC 797  
 481 GCTCGAATCTGTATTGGAAACACCTTACTACCTGTCCCCAGAGATCTGTGAGAAATAAACC 540  
 798 GCTCGAATCTGTATTGGAAACACCTTACTACCTGTCCCCAGAGATCTGTGAGAAATAAACC 857  
 541 TACCAAAATAAAGCGATATTGGTCTCTTGGCTGTGCTTATATAGAGCTCTGCACTT 600  
 858 TACCAAAATAAAGCGATATTGGTCTCTTGGCTGTGCTTATATAGAGCTCTGCACTT 917  
 601 AAACATCTCTTTGAGGGTAAACACTTACAGAGCTGGTTCTGAAAGATTGTCAAGACAT 660  
 918 AAACATCTCTTTGAGGGTAAACACTTACAGAGCTGGTTCTGAAAGATTGTCAAGACAT 977  
 661 TTGCCCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 978 TTGCCCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT 1037  
 721 CAAGTATCTCTCGAGCCGACCATCCATAAATTCATTTCCAAAGGCCCTTTTAGAG 780  
 1038 CAAGTATCTCTCGAGCCGACCATCCATAAATTCATTTCCAAAGGCCCTTTTAGAG 1097  
 781 AATCTTATCCCAATATTGACTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTT 840  
 1098 AATCTTATCCCAATATTGACTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTT 1157  
 841 ATATGAGAGAGGAGCGCCAGCTCTCGACATGCTGGGAAGGTGGTCCAGAGGTGAAA 900  
 1158 ATATGAGAGAGGAGCGCCAGCTCTCGACATGCTGGGAAGGTGGTCCAGAGGTGAAA 1217  
 901 ATACAAAAAGTGAGATTCCAGGGAAGTGCCCAACCAAGATCAAGGATATCTGTGCAATT 960  
 1218 ATACAAAAAGTGAGATTCCAGGGAAGTGCCCAACCAAGATCAAGGATATCTGTGCAATT 1277  
 961 AAAAGGAATGCTATATTGATAGAAATGATGGAGACCAAGCTGGAGCCAGAGGCC 1020  
 1278 AAAAGGAATGCTATATTGATAGAAATGATGGAGACCAAGCTGGAGCCAGAGGCC 1337  
 1021 AGATCTATAAAATGATAGAAAGACCCAAATTTGCTGTCTGTGGACATTATGATTAT 1080  
 1338 AGATCTATAAAATGATAGAAAGACCCAAATTTGCTGTCTGTGGACATTATGATTAT 1397  
 1081 TATTATGCTCAACTTGTATGCTGAGGAGAGAGGCCCAAAACCAAGTTATCACCTATT 1140  
 1398 TATTATGCTCAACTTGTATGCTGAGGAGAGAGGCCCAAAACCAAGTTATCACCTATT 1457  
 1141 CCTCAAGAAATACCTGGGCTTGGAGATTACGCTCAGGAACAGGATGGTCCATCCCA 1200  
 1458 CCTCAAGAAATACCTGGGCTTGGAGATTACGCTCAGGAACAGGATGGTCCATCCCA 1517  
 1201 AGTCAATGGCCTGCTGAGTACCTTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1260  
 1518 AGTCAATGGCCTGCTGAGTACCTTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1577  
 1261 GTGGAGAACCAATTTGGTCTTGTGCTTCTTCTGGAGCCAAATACACAGAGACAA 1320  
 1578 GTGGAGAACCAATTTGGTCTTGTGCTTCTTCTGGAGCCAAATACACAGAGACAA 1637  
 1321 GAGCTAAGAAATTAATGGAGAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA 1380  
 1638 GAGCTAAGAAATTAATGGAGAGAGCCTAGATTCCAGGAGCTGCCATTTAGGAAAAACGAA 1697  
 1381 ATGAAGGAACAGGAATATTGGAGAGAGCTTAGAGGAAATACGCCAACAGTACCAATGAC 1440  
 1698 ATGAAGGAACAGGAATATTGGAGAGAGCTTAGAGGAAATACGCCAACAGTACCAATGAC 1757  
 1441 ATGAAGGAATTAAGAAAGAGATGGGAGAGAACCCAGAGGAGAACTCAAAAATTAAGTAT 1500

1758 ATGAAGAAATTAAGAAAGAGATGGGAGAGAACCCAGAGAGAACTCAAAAATTAAGTCAT 1817  
 1501 AAAACCTTATTGGTGAAGAAAGATTAACCTGCTCCATCAAGATGATCTGAGGGAGAA 1560  
 1818 AAAACCTTATTGGTGAAGAAAGATTAACCTGCTCCATCAAGATGATCTGAGGGAGAA 1877  
 1561 GCACCTGTGAGGACATTTGAAAAGACTTTGAAAACAAATGAGGCTTCAGAACACAAAGGAA 1620  
 1878 GCACCTGTGAGGACATTTGAAAAGACTTTGAAAACAAATGAGGCTTCAGAACACAAAGGAA 1937  
 1621 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGTAAAAATTTGAAAATTAATTTA 1680  
 1938 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGTAAAAATTTGAAAATTAATTTA 1997  
 1681 GACAAATGTATTTCTGATGAAAACATCTCCAGAGAGAAAGCAATGATATACCAAAAT 1740  
 1998 GACAAATGTATTTCTGATGAAAACATCTCCAGAGAGAAAGCAATGATATACCAAAAT 2057  
 1741 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAAGAAATATGAATGTTTAAAGGAGCAT 1800  
 2058 GAAACTTTGACCTTTGAGGATGGCATGAAGTTTAAAGAAATATGAATGTTTAAAGGAGCAT 2117  
 1801 GGAGATTATACAGACAAAGCATTTTGAATAATTTGAAAACATTTCACTGCCAGAGAGGCTTTCCACG 1860  
 2118 GGAGATTATACAGACAAAGCATTTTGAATAATTTGAAAACATTTCACTGCCAGAGAGGCTTTCCACG 2177  
 1861 CAGACTGTAGCTGCTGTGGGAAACAGGAGGAGTGGATGGAGGAGGCGCTCAGACTCTG 1920  
 2178 CAGACTGTAGCTGCTGTGGGAAACAGGAGGAGTGGATGGAGGAGGCGCTCAGACTCTG 2237  
 1921 CTGCAGATGATGGCAGTGGCGGACATCACTCCACCTGCCCGGCGGCTGACAGTG 1978  
 2238 CTGCAGATGATGGCAGTGGCGGACATCACTCCACCTGCCCGGCGGCTGACAGTG 2295

RESULT 4  
 ABK12425

ID ABK12425 standard; cDNA; 1965 BP.

XX AC ABK12425;

XX DT 18-JUN-2002 (first entry)

XX DE cDNA encoding novel human kinase protein #2.

XX KW Novel human protein; NHP; serine-threonine kinase; brain;  
 KW calcium/calmodulin-dependent kinase; myosin light chain kinase;  
 KW biological disorder; spleen; placenta; chromosome 6; gene; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT CDS 1..1965

XX FT /\*tag= a

XX FT /product= "Human kinase protein #2"

XX WO200218555-A2.

XX PN 07-MAR-2002.

XX PD 28-AUG-2001; 2001WO-US026776.

XX PF 31-AUG-2000; 2000US-0229280P.

XX PR (LEXI-) LEXICON GENETICS INC.

XX PI Friddle CJ, Hilbun E, Nepomnichy B, Hu Y;

XX XX WPI; 2002-292200/33.

XX DR P-ESDB; AAU77929.

XX PT Novel polynucleotide encoding novel human protein sharing structural  
 PT similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-



PT dependent, and myosin light chain kinases, useful as probes and primers.  
 XX Disclosure; Page 39-40; 46pp; English.  
 PS The present invention relates to the isolation of novel human proteins  
 CC (NHPs) and the polynucleotide sequences encoding them. The NHPs of the  
 CC invention are kinase proteins and share structural similarity to serine-  
 CC threonine, calcium/calmodulin-dependent, and myosin light chain kinases.  
 CC The sequences of the invention are useful for treating biological  
 CC disorders. The polynucleotide sequences encoding the kinase proteins can  
 CC be used as primers and probes. The sequences are also useful for  
 CC identifying mutations associated with a particular disease and also in a  
 CC prognostic or diagnostic assay. The present sequence encodes human  
 CC protein kinase #2 which is expressed in a broad range of human tissues  
 CC such as brain, spleen, and placenta. The gene encoding protein kinase #2  
 CC is located on chromosome 6  
 XX Sequence 1965 BP; 658 A; 377 C; 458 G; 472 T; 0 U; 0 Other;

Query Match 91.0%; Score 1868; DB 6; Length 1965;  
 Best Local Similarity 95.8%; Pred. No. 0;  
 Matches 1965; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
 QY 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGGTGCTTCGGGAAAGCATCTTA 60  
 DB 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGGTGCTTCGGGAAAGCATCTTA 60  
 QY 61 GCTAAGGGAATCAGATAGCAAGCACTGTGTCATTAAGAGATCAATTTGAAAGATG 120  
 DB 61 GCTAAGGGAATCAGATAGCAAGCACTGTGTCATTAAGAGATCAATTTGAAAGATG 120  
 QY 121 CCCATACAAAGAAAGAGCTTCAAGAAAGAGTGTCTTCGAAAGATCAAAAT 180  
 DB 121 CCCATACAAAGAAAGAGCTTCAAGAAAGAGTGTCTTCGAAAGATCAAAAT 180  
 QY 181 CCCAATGTAGCTTCTTCAATTCATTTCAAGAGAAATGCGAGTGTATTTT 240  
 DB 181 CCCAATGTAGCTTCTTCAATTCATTTCAAGAGAAATGCGAGTGTATTTT 240  
 QY 241 GAATATTGTAGTGGAGGATCTCATGAAAGAGTCAATAGCAACGGGGTGTATTT 300  
 DB 241 GAATATTGTAGTGGAGGATCTCATGAAAGAGTCAATAGCAACGGGGTGTATTT 300  
 QY 301 AGTGAAGATCAGATCTCGGTGGTTGTACAGATTTCTTAGCACTAAATCATATT 360  
 DB 301 AGTGAAGATCAGATCTCGGTGGTTGTACAGATTTCTTAGCACTAAATCATATT 360  
 QY 361 GACGGAAGATATTACAGGAGATTAAGCTCAGACATTTCTTAGCAAGACGGA 420  
 DB 361 GACGGAAGATATTACAGGAGATTAAGCTCAGACATTTCTTAGCAAGACGGA 420  
 QY 421 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATTAATTCAGAACTT 480  
 DB 421 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCTCTGAATTAATTCAGAACTT 480  
 QY 481 GTCGAACCTTGTATTGGAAACCTTACTACCTGTCCCGAGAGATCTGTGAGAAATTAACCC 540  
 DB 481 GTCGAACCTTGTATTGGAAACCTTACTACCTGTCCCGAGAGATCTGTGAGAAATTAACCC 540  
 QY 541 TACAACATTAACCGGATTTGGTCTCTGGCTGTGCTTATATGAGCTCTGACACATTT 600  
 DB 541 TACAACATTAACCGGATTTGGTCTCTGGCTGTGCTTATATGAGCTCTGACACATTT 600  
 QY 601 AAACATCTTTTGGAGGTAAACACTTACAGAGTGTGTTTGAAGATTTGTCAAGACAT 660  
 DB 601 AAACATCTTTTGGAGGTAAACACTTACAGAGTGTGTTTGAAGATTTGTCAAGACAT 660  
 QY 661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 DB 661 TTTGCCCAATATCTCCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 QY 721 CAAGTATCTCTCGAGACCGACCATTCATTAATTCATTTTGAAGAGCCCTTTTAGAG 780

Db 721 CAAGTATCTCTCGAGACCGACCATCCATTAATTCATTTTGAAGAGCCCTTTTAGAG 780  
 QY 781 AATCTTTATTTCCAAATATTTTGAATCTCTGAGGTCAATTCAGGAAGAAATTCAGTCACTGCTT 840  
 Db 781 AATCTTTATTTCCAAATATTTTGAATCTCTGAGGTCAATTCAGGAAGAAATTCAGTCACTGCTT 840  
 QY 841 ATATGAGAGCAGAGGAGCCAGCTTCTCGACATGCTGGGAAGTGTCCAGAAAGTGTAAA 900  
 Db 841 ATATGAGAGCAGAGGAGCCAGCTTCTCGACATGCTGGGAAGTGTCCAGAAAGTGTAAA 900  
 QY 901 ATACAAAAGTGAATTCAGGGAAGTCCCAACCAAGATCAAGGATATCTGTGCAAT 960  
 Db 901 ATACAAAAGTGAATTCAGGGAAGTCCCAACCAAGATCAAGGATATCTGTGCAAT 960  
 QY 961 AAAAGGAATGCTATATTGATAGAAATGAATGGAGACCAACCAAGCTGGAGCCAGAGGCC 1020  
 Db 961 AAAAGGAATGCTATATTGATAGAAATGAATGGAGACCAACCAAGCTGGAGCCAGAGGCC 1020  
 QY 1021 AGATCTATAAAATGATAGAAAGACCCAAATTTGCTGTCTGTGACATTAATGATTAT 1080  
 Db 1021 AGATCTATAAAATGATAGAAAGACCCAAATTTGCTGTCTGTGACATTAATGATTAT 1080  
 QY 1081 TATTATGCTCAACTTGTAGTATGCTGAGGAGAGGCCCAACCAAGTTTATCACCTTAT 1140  
 Db 1081 TATTATGCTCAACTTGTAGTATGCTGAGGAGAGGCCCAACCAAGTTTATCACCTTAT 1140  
 QY 1141 CCTCAAGAAATACCTGAGTTCAGGATTAACGCTCAGGAACGAGCATGCTCCATCCCA 1200  
 Db 1141 CCTCAAGAAATACCTGAGTTCAGGATTAACGCTCAGGAACGAGCATGCTCCATCCCA 1200  
 QY 1201 AGTCAATGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACATATTAAGTTGAA 1260  
 Db 1201 AGTCAATGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACATATTAAGTTGAA 1260  
 QY 1261 GTGGAGAACCAATGGTCTTCTGTCATCTTCTCGAGCCAAATTCACACAGAGACAA 1320  
 Db 1261 GTGGAGAACCAATGGTCTTCTGTCATCTTCTCGAGCCAAATTCACACAGAGACAA 1320  
 QY 1321 GAGCTAAGAAATTAAGGAGAGGCTAGATTCAGAGAGCTGCCATTTAGGAAACCGAA 1380  
 Db 1321 GAGCTAAGAAATTAAGGAGAGGCTAGATTCAGAGAGCTGCCATTTAGGAAACCGAA 1380  
 QY 1381 ATGAAGGAACAGGAATATTGGAGCAGTTAGAGAAATACGCCAAGTACCAATGAC 1440  
 Db 1381 ATGAAGGAAC----- 1390  
 QY 1441 ATGAAGGAATTAGAAAGAGATGGGAGAGAACCCAGAGGAGAACTCAAAAATAAGTCAT 1500  
 Db 1391 -----AGGAACTCAAAAATAAGTCAT 1413  
 QY 1501 AAAACCTATTGGTGAAGAGATTAACCTGCTGTCATCAAGATGCAATCTGAGGAGAA 1560  
 Db 1414 AAAACCTATTGGTGAAGAGATTAACCTGCTGTCATCAAGATGCAATCTGAGGAGAA 1473  
 QY 1561 GCACCTGTCAGGACATTCGAAAGAGCTTGAACAAATGAGGCTTCAGAACCAAGGAA 1620  
 Db 1474 GCACCTGTCAGGACATTCGAAAGAGCTTGAACAAATGAGGCTTCAGAACCAAGGAA 1533  
 QY 1621 AGTAAATAATCCAGAACAGAAATATAAGCTAAGAGGGGGTAAAAATTTGAAATTAATTTA 1680  
 Db 1534 AGTAAATAATCCAGAACAGAAATATAAGCTAAGAGGGGGTAAAAATTTGAAATTAATTTA 1593  
 QY 1681 GACAAATGATTCTGATGAAGAACATCTCCAGAGAGAGAGGCAATGATATACAAAT 1740  
 Db 1594 GACAAATGATTCTGATGAAGAACATCTCCAGAGAGAGAGGCAATGATATACAAAT 1653  
 QY 1741 GAACTTTGACCTTTGAGGATGGCATGAAGTTTAAAGGAATATGAATGTCTAAAGGAGCAT 1800  
 Db 1654 GAACTTTGACCTTTGAGGATGGCATGAAGTTTAAAGGAATATGAATGTCTAAAGGAGCAT 1713  
 QY 1801 GGAGATATTACAGAACAGCATTTGAAAAAATTTCTACTGCCAGAGAGCGGTTTCCAGG 1860  
 Db 1714 GGAGATATTACAGAACAGCATTTGAAAAAATTTCTACTGCCAGAGAGCGGTTTCCAGG 1773

Qy	1861	CAGACTGTAGTCTGTGGGAAACAGAGGCGAGTGGATGGAGAGCGCTTCAGACTCTG	1920
Db	1774	CAGACTGTAGTCTGTGGGAAACAGAGGCGAGTGGATGGAGAGCGCTTCAGACTCTG	1833
Qy	1921	CTGCAGATGATGGCAGTGGCCGACATCACCTGCCACGGGGCTGCACAGTGAG	1980
Db	1834	CTGCAGATGATGGCAGTGGCCGACATCACCTGCCACGGGGCTGCACAGTGAG	1893
Qy	1981	TCTGTGTTAGCGTCAGTCTCAGGAAGGAAGCAAGGACCCGTACAGCCCACTGCTC	2040
Db	1894	TCTGTGTTAGCGTCAGTCTCAGGAAGGAAGCAAGGACCCGTACAGCCCACTGCTC	1953
Qy	2041	ATCCTGATGTGA	2052
Db	1954	ATCCTGATGTGA	1965

5 T. WISSEBACH

ABS57149

ID AB857149 standard: cDNA: 2370 bp.

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PR 05-11

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CC The

CC carcinoma). Agents which modulate the function or activity of the protein  
CC are useful to treat diseases or disorders mediated by human kinase  
CC protein. The gene for encoding the novel kinase is located on chromosome  
CC 13. The present sequence is the cDNA encoding the novel human kinase  
XX.  
SQ Sequence 2370 BP; 796 A; 456 C; 550 G; 568 T; 0 U; 0 Other;

Db 912 ATACAAAAAGTGAGATTCGGGGAAGTGCCACCAAGATCAAGGATATCTGTGCCAATT 971

Qy 961 AAAAGGAATGCTATATTCATAGAAATGAATGGAGACCCAGCTGGAGCCCAAGGCC 1020

Db 972 AAAAGGAATGCTATATTCATAGAAATGAATGGAGACCCAGCTGGAGCCCAAGGCC 1031

Qy 1021 AGATCTATAAAAAATGATAGAAAGACCCAAAATTTGCTGCTGTGTGACATTAATGATAT 1080

Db 1032 AGATCTATAAAAAATGATAGAAAGACCCAAAATTTGCTGCTGTGTGACATTAATGATAT 1091

Qy 1081 TATTATGCTCAACTTGTATATGCTGAGGAGAGAGCCCAAAACCAAGTTATCACCTTATT 1140

Db 1092 TATTATGCTCAACTTGTATATGCTGAGGAGAGAGCCCAAAACCAAGTTATCACCTTATT 1151

Qy 1141 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTACAGGAAGAGGCGATGTCCTATCCCA 1200

Db 1152 CCTCAAGAAAATACTGGAGTTGAGGATTACGGTACAGGAAGAGGCGATGTCCTATCCCA 1211

Qy 1201 AGTCAATGGCTGTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1260

Db 1212 AGTCAATGGCTGTGAGTACCTTCAGAGAAAATTTGAAGCTCAACAATATAAGTTGAAA 1271

Qy 1261 GTGGAGAGCAATTTGGTCTGCTCCATCTTCTCGGAGCCAAATTAACAACAGAGACAA 1320

Db 1272 GTGGAGAGCAATTTGGTCTGCTCCATCTTCTCGGAGCCAAATTAACAACAGAGACAA 1331

Qy 1321 GAGCTAAGAAGTAATGAGAGAGAGCTAGATTCCAGAGAGCTGCCATTTAGAAAAGCAA 1380

Db 1332 GAGCTAAGAAGTAATGAGAGAGAGCTAGATTCCAGAGAGCTGCCATTTAGAAAAGCAA 1391

Qy 1381 ATGAGAGACAGGAATATTGAGAGAGTTAGAGGAATACCCCAACAGTACCAATGAC 1440

Db 1392 ATGAGAGACAGGAATATTGAGAGAGTTAGAGGAATACCCCAACAGTACCTCAATGAC 1451

Qy 1441 ATGAGAGAAATTTAGAAAAGATGGGAGAGAACCCAGAGGAGAACTCAAAAATAAGTCAT 1500

Db 1452 ATGAGAGAAATTTAGAAAAGATGGGAGAGAACCCAGAGGAGAACCCAGAGGAGAAC 1488

Qy 1501 AAAACCTATTTGTTGAGAGAGAGTAACCTGCTGTCCATCAAGATGCAATCTGAGGGAGAA 1560

Db 1489 ----- 1488

Qy 1561 GCACCTGTGCAGGACATTTGAAAAGAGCTTGAACAAATGAGGCTTCAGAACACAAAGGAA 1620

Db 1489 -----AGGACATTTGAAAAGAGCTTGAACAAATGAGGCTTCAGAACACAAAGGAA 1538

Qy 1621 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGGTAAATTTGAAATTAATTA 1680

Db 1539 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAGGGGGTAAATTTGAAATTAATTA 1598

Qy 1681 GACAAATGATTTCTGATGAACATCTCCAGAGGAGGCAATGATATACCAAT 1740

Db 1599 GACAAATGATTTCTGATGAACATCTCCAGAGGAGGCAATGATATACCAAT 1658

Qy 1741 GAAACTTTGACCTTTGAGGATGCGATGAAGTTTAAAGGAATATGAATGTGTAAGAGGACAT 1800

Db 1659 GAAACTTTGACCTTTGAGGATGCGATGAAGTTTAAAGGAATATGAATGTGTAAGAGGACAT 1718

Qy 1801 GGAGATTATACAGACAAAGCAATTTGAAAACCTTCACTGCCAGAGCAGGGTTTCCAG 1860

Db 1719 GGAGATTATACAGACAAAGCAATTTGAAAACCTTCACTGCCAGAGCAGGGTTTACAGAA 1778

Qy 1861 CAGACT 1866

Db 1779 CTGACT 1784

RESULT 6

AAS06745

ID AAS06745 standard; cDNA; 1947 BP.

XX

AC

XX AAS06745;

DT 12-SEP-2001 (first entry)

XX Polynucleotide sequence encoding human protein kinase #45.

DE Human; protein kinase; PKK; STK; cancer; cardiovascular disease;

XX Metabolic disorder; immune related disease; neurological disorder;

KW neurodegenerative disorder; inflammatory disorder; infectious disease;

KW reproductiv disorder; gene therapy; ss.

XX Homo sapiens.

OS

XX MO200138503-A2.

FN

XX 31-MAY-2001.

PD

XX 22-NOV-2000; 2000WO-US032085.

PF

XX 24-NOV-1999; 99US-0167482P.

XX (SUGSE-) SUGEN INC.

XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

PI Flanagan P, Clary D;

PI

XX WPI; 2001-343950/36.

DR

XX P-PSDB; AAU03545.

XX Nucleic acids encoding human kinase polypeptides, useful for preventing

PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and

PT neuronal-associated diseases, and microbial infections.

XX

PS Example 1; Fig 1; 433pp; English.

XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel

CC protein kinases have been identified as members of the tyrosine or

CC serine/threonine kinase (PTK and STK) families. The polynucleotides

CC encoding protein kinases and the polypeptides may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate kinase expression. For example, they may be used to treat

CC cancers (especially cancers of haematopoietic origin), cardiovascular

CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),

CC immune related diseases (e.g. rheumatoid arthritis), neurological

CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.

CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious

CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).

CC Additionally, polynucleotides encoding protein kinases may be used for

CC gene therapy and as DNA probes in diagnostic assays. The protein kinase

CC polypeptides may be used as antigens in the production of antibodies

CC against the protein kinases and in assays to identify modulators of

CC protein kinase expression and activity

XX

SQ Sequence 1947 BP; 638 A; 357 C; 455 G; 497 T; 0 U; 0 Other;

Query Match 71.6%; Score 1469.6; DB 4; Length 1947;

Best Local Similarity 87.0%; Pred. NC. 0;

Matches 1721; Conservative 0; Mismatches 89; Indels 168; Gaps 3;

Qy 1 ATGGATAAGTACGATGATTAAGGCCCATCGGCAAGTGCTTCGGAAAGCATACTTA 60

Db 1 ATGGATAAGTACGATGATTAAGGCCCATCGGCAAGTGCTTCGGAAAGCATACTTA 60

Qy 61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTGAAAGATG 120

Db 61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTGAAAGATG 120

Qy 121 CCCATACAGAAAAGAGAGCTTCAAGAGAGAGTGATCTCTCGAAAAGATGAACAT 180

Db 121 CCCATACAGAAAAGAGAGCTTCAAGAGAGAGTGATCTCTCTCGAAAAGATGAACAT 180

Qy 181 CCCAATTTGTAGCTTCTTCAATTCATTTCAAGAGAGATGCGAGGCTTTTATGTAATG 240

Db 181 CCCAATTTGTAGCTTCTTCAATTCATTTCAAGAGAGATGCGAGGCTTTTATGTAATG 240



XX PA (FARB ) BAYER AG.  
XX PI Xiao Y;  
XX DR WPI: 2003-184051/18.  
XX DR P-PSDB; ABP71710.  
XX PT New polynucleotide encoding a NEK-like serine/threonine kinase  
XX PT polypeptide useful for treating diseases associated with kinase  
XX PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,  
XX PT diabetes and CNS disorders.  
XX PS Claim 1 b; Fig 1; 149pp; English.  
XX CC The invention relates to a newly isolated polynucleotide encoding an NEK-  
CC like serine/threonine protein kinase. The activity of the polynucleotide  
CC and polypeptide of the invention may be described as cytostatic,  
CC cardiant, antiinflammatory, nootropic and neuroprotective. The expression  
CC vector and reagent of the invention are useful for the preparation of a  
CC medicament for modulating the activity of an NEK-like serine/threonine  
CC kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular  
CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be  
CC used to identify compounds which may act as activators or inhibitors at  
CC the enzyme's active site, to raise specific antibodies which can block  
CC the enzyme and effectively reduce its activity, as a bait protein in a  
CC two-hybrid or three-hybrid assay to identify other proteins which bind to  
CC or interact with the human NEK-like serine/threonine kinase polypeptide  
CC and modulate its activity, and for the immunisation of mammals. The  
CC current sequence represents the human NEK-like serine/threonine protein  
CC kinase encoding DNA  
XX CC  
XX SQ Sequence 1896 BP; 608 A; 350 C; 455 G; 473 T; 0 U; 0 Other;

Query Match 66.3%; Score 1359.8; DB 8; Length 1896;  
Best Local Similarity 84.5%; Pred. No. 0;  
Matches 1673; Conservative 0; Mismatches 82; Indels 224; Gaps 4;

QY 1 ATGGATAGTACGATGATTAAGGCCATCGGCAAGTGCTTCGGGAAGCATCTTA 60  
DB |||||||  
QY 1 ATGGATAGTACGATGATTAAGGCCATCGGCAAGTGCTTCGGGAAGCATCTTA 60  
DB |||||||  
QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTCTATAAAGAGATCAATTTTGAAGATG 120  
DB |||||||  
QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTCTATAAAGAGATCAATTTTGAAGATG 120  
DB |||||||  
QY 121 CCATACAGAAAGAGCTTCAAGAAAGAGTCTTCTGGAAGAGATGAAACAT 180  
DB |||||||  
QY 121 CCATACAGAAAGAGCTTCAAGAAAGAGTCTTCTGGAAGAGATGAAACAT 180  
DB |||||||  
QY 181 CCCAATTTGTAGCTTCTCAATTCATTTCAAGAGATGCGAGCTGTTTATGTAATG 240  
DB |||||||  
QY 181 CCCAATTTGTAGCTTCTCAATTCATTTCAAGAGATGCGAGCTGTTTATGTAATG 240  
DB |||||||  
QY 241 GAATATTGTAGTGGAGGATCTCATGAAGAGATCAATGACAAACGGGGTGTATTT 300  
DB |||||||  
QY 241 GAATATTGTAGTGGAGGATCTCATGAAGAGATCAATGACAAACGGGGTGTATTT 300  
DB |||||||  
QY 301 AGTGAAGATCAGATCCTCGGTGGTTTGTACAGATTTCTTAGACTTAAACATATTCAT 360  
DB |||||||  
QY 301 AGTGAAGATCAGATCCTCGGTGGTTTGTACAGATTTCTTAGACTTAAACATATTCAT 360  
DB |||||||  
QY 361 GACAGGAAGATATACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 420  
DB |||||||  
QY 361 GACAGGAAGATATACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 420  
DB |||||||  
QY 421 ATGGTGGCAAGCTTTGGGACTTTGGTATACAGAGTCTTGAATATTCATCGAACTT 480  
DB |||||||  
QY 421 ATGGTGGCAAGCTTTGGGACTTTGGTATACAGAGTCTTGAATATTCATCGAACTT 480  
DB |||||||  
QY 481 GCTCGAATCTGTATGGAACACCTTACTACCTGTCCCGAGAGATCTGTGAGAATAAACC 540  
DB |||||||  
QY 481 GCTCGAATCTGTATGGAACACCTTACTACCTGTCCCGAGAGATCTGTGAGAATAAACC 540  
DB |||||||

QY 541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGCTTATATAGACTCTGCACATTT 600  
DB |||||||  
QY 541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGCTTATATAGACTCTGCACATTT 600  
DB |||||||  
QY 601 AAACATCCTTTTGAGGTAAACAACCTACAGCAGCTGGTCTGAAGATTTGCAACACAT 660  
DB |||||||  
QY 601 AAACATCCTTTTGAGGTAAACAACCTACAGCAGCTGGTCTGAAGATTTGCAACACAT 660  
DB |||||||  
QY 661 TTGGCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
DB |||||||  
QY 661 TTGGCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
DB |||||||  
QY 721 CAAGTATCTCTCGAGACCGACATCCATAAATTCATTTGAAAAGGCCCTTTTAGAG 780  
DB |||||||  
QY 721 CAAGTATCTCTCGAGACCGACATCCATAAATTCATTTGAAAAGGCCCTTTTAGAG 780  
DB |||||||  
QY 781 AATCTTATTTCCCAATATTTGACTCTCTGAGGTCAATTCAGGAAGAATTCAGTCACATGTT 840  
DB |||||||  
QY 781 AATCTTATTTCCCAATATTTGACTCTCTGAGGTCAATTCAGGAAGAATTCAGTCACATGTT 840  
DB |||||||  
QY 841 ATATGACAGCAGGAGCGCCAGCTTCTCGACATGTCTGGGAAGTGTCTCAGAGTGA-A 899  
DB |||||||  
QY 841 ATATGACAGCAGGAGCGCCAGCTTCTCGACATGTCTGGGAAGTGTCTCAGAGGATACT 900  
DB |||||||  
QY 900 AATACAAAAGTGAGATTCACAGGAAAGTGCCCAACAGATCAAGATATCTGTGCCAAT 959  
DB |||||||  
QY 901 GGTGTGAGGAGTGGCTCTCAAGGCTTGGGAGCTCTGCTCTGAGGCTTTGAGGCTA 960  
DB |||||||  
QY 960 TAAAGGAATGCTATATTTGATAGAAATGAATGGAGACCAACAGCTGGAGCCAGAGGC 1019  
DB |||||||  
QY 961 CAGCCCTCGGCTGCTCTCACAGG-----CTGCTGTGAGTGTCTGGGCT 1007  
DB |||||||  
QY 1020 CAGATCTATAAAATCATAGAAAGACCCAAATTTGCTGCTGTGACATTTAGTTA 1079  
DB |||||||  
QY 1008 TTTCAGATATAAAATCATAGAAAGACCCAAATTTGCTGCTGTGACATTTAGTTA 1067  
DB |||||||  
QY 1080 TTATATGCTCAACTTGTATATGCTGAGGAGAGAGCCCAACCAAGTTATCACCTAT 1139  
DB |||||||  
QY 1068 TTATATGCTCAACTTGTATATGCTGAGGAGAGAGCCCAACCAAGTTATCACCTAT 1127  
DB |||||||  
QY 1140 TCTTCAAGAAATATCTGAGTTGAGATTAACGTCAGGAACAGAGGATGTCCATCCCC 1199  
DB |||||||  
QY 1128 TCTTCAAGAAATATCTGAGTTGAGATTAACGTCAGGAACAGAGGATGTCCATCCCC 1187  
DB |||||||  
QY 1200 AAGTCAATGCTGCTGAGTACCTTCAAGAAATTTGAGCTCAACATATAAGTTGAA 1259  
DB |||||||  
QY 1188 AAGTCAATGCTGCTGAGTACCTTCAAGAAATTTGAGCTCAACATATAAGTTGAA 1247  
DB |||||||  
QY 1260 AGTGGAGAAAGCAATTTGGTCTTCTGCTCCATTTCTCCGAGGCCAAATTCACCCAGAGACA 1319  
DB |||||||  
QY 1248 AGTGGAGAAAGCAATTT----- 1262  
DB |||||||  
QY 1320 AGAGCTAAGAAATAGGAGAGAGCTTAGATTTCCAGGAGCTGCCATTTAGGAAAAACA 1379  
DB |||||||  
QY 1263 ----- 1262  
DB |||||||  
QY 1380 AATGAGGAACAGGAATATTGGAAGCAGTTAGAGAAATAGCCAAACAGTACCAATGA 1439  
DB |||||||  
QY 1263 -----GGAATATTGGAAGCAGTTAGAGAAATAGCCAAACAGTACCAATGA 1310  
DB |||||||  
QY 1440 CATGAAGAATATGAGGAAGATGGGAGAGAAACAGAGGAGACTCAAAATTAAGTCA 1499  
DB |||||||  
QY 1311 CATGAAGAATATGAGGAAGATGGGAGAGAAACAG----- 1348  
DB |||||||  
QY 1500 TAAACCTATTTGGTGAAGAGAGATAA CCTGCTCTCCATCAAGATGATCTGTAGGGAGA 1559  
DB |||||||  
QY 1349 ----- 1348  
DB |||||||  
QY 1560 AGCAGCTGTGAGGACATTTGAAAAAGACTTGAAACAAATGAGGCTTCAGAACACAAAGGA 1619  
DB |||||||  
QY 1349 -----AGGACATTTGAAAAAGACTTTGAAACAAATGAGGCTTCAGAACACAAAGGA 1397  
DB |||||||

QY 1620 AAGTAAATCCAGACACAAATATAAGCTAAGAGGGGTAAATTTGAAATTAATTT 1679  
 Db 1398 AAGTAAATCCAGACACAAATATAAGCTAAGAGGGGTAAATTTGAAATTAATTT 1457  
 QY 1680 AGACAAATGATTTCTGATGAAACATCTCCAGAGGAGGCAATGGATATACCAA 1739  
 Db 1458 AGACAAATGATTTCTGATGAAACATCTCCAGAGGAGGCAATGGATATACCAA 1517  
 QY 1740 TGAACCTTTGACCTTTGAGATGGCATGAAGTTTAAGGAATATGAATGTGTAAGAGGCA 1799  
 Db 1518 TGAACCTTTGACCTTTGAGATGGCATGAAGTTTAAGGAATATGAATGTGTAAGAGGCA 1577  
 QY 1800 TGGAGATTATACAGACAAAGCAATTTGAAAACTTCACTGCCAGAGGAGGGTTTTCCAC 1859  
 Db 1578 TGGAGATTATACAGACAAAGCAATTTGAAAACTTCACTGCCAGAGGAGGGTTTTCCAC 1637  
 QY 1860 GCAGACTGTAGCTGTGGGAAACAGAGGAGGAGTGGGATGAGAGGCGCTCAGACTCT 1919  
 Db 1638 GCAGACTGTAGCTGTGGGAAACAGAGGAGGAGTGGGATGAGAGGCGCTCAGACTCT 1697  
 QY 1920 GTTCGAGATGATGGCAGTGGCGACATCACCTCCACCTGCCCGCCAGGCGCTGACAGTG 1978  
 Db 1698 GTTCGAGATGATGGCAGTGGCGACATCACCTCCACCTGCCCGCCAGGCGCTGACAGTG 1756

RESULT 8

ABZ59717  
 ID ABZ59717 standard; DNA; 1918 BP.

AC ABZ59717;

XX 17-APR-2003 (first entry)

DE Human NEK-like serine/threonine protein kinase DNA # SEQ ID 4.

XX Human; NEK-like serine/threonine protein kinase; cytostatic; cardiant;  
 KW antiinflammatory; nootropic; neuroprotective; cancer; colon cancer;  
 KW cardiovascular disorder; diabetes; COPD; CNS disorder; ds.  
 XX Homo sapiens.

XX WO2003000903-A2.

XX 03-JAN-2003.

XX 24-JUN-2002; 2002WO-BP06948.

XX 25-JUN-2001; 2001US-0300068P.

XX 07-DEC-2001; 2001US-0336704P.

XX (FARB ) BAYER AG.

XX Xiao Y;

XX WPI; 2003-184051/18.

XX New polynucleotide encoding a NEK-like serine/threonine kinase  
 PT polypeptide useful for treating diseases associated with kinase  
 PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,  
 PT diabetes and CNS disorders.  
 XX Disclosure; Fig 4; 149pp; English.

XX The invention relates to a newly isolated polynucleotide encoding an NEK-  
 CC like serine/threonine protein kinase. The activity of the polynucleotide  
 CC and polypeptide of the invention may be described as cytostatic,  
 CC cardiant, antiinflammatory, nootropic and neuroprotective. The expression  
 CC vector and reagent of the invention are useful for the preparation of a  
 CC medicament for modulating the activity of an NEK-like serine/threonine  
 CC kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular  
 CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be  
 CC used to identify compounds which may act as activators or inhibitors at  
 CC the enzyme's active site, to raise specific antibodies which can block

CC the enzyme and effectively reduce its activity, as a bait protein in a  
 CC two-hybrid or three-hybrid assay to identify other proteins which bind to  
 CC or interact with the human NEK-like serine/threonine kinase polypeptide  
 CC and modulate its activity, and for the immunisation of mammals. The  
 CC current sequence represents human NEK-like serine/threonine protein  
 CC kinase encoding DNA  
 XX  
 SQ Sequence 1918 BP; 615 A; 367 C; 460 G; 476 T; 0 U; 0 Other;

Query Match 66.3%; Score 1359.8; DB 8; Length 1918;  
 Best Local Similarity 84.5%; Pred. No. 0;  
 Matches 1673; Conservative 0; Mismatches 82; Indels 224; Gaps 4;

QY 1 ATGGATTAAGTACGATGTGATTAAAGCCATCGGCAAGGTGCTTCGGGAAGCATACTTA 60  
 Db 23 ATGGATTAAGTACGATGTGATTAAAGCCATCGGCAAGGTGCTTCGGGAAGCATACTTA 82  
 QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTTGAAGAAGTG 120  
 Db 83 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTTGAAGAAGTG 142  
 QY 121 CCATACAGAAAGAGAGCTTCAAGAAAGAGTGTCTTCTGGAAGAGATGAACAT 180  
 Db 143 CCCATACAGAAAGAGAGCTTCAAGAAAGAGTGTCTTCTGGAAGAGATGAACAT 202  
 QY 181 CCCAACATTTAGTCTTCTTCAATTTCAAGAGAAATGCGAGGCTGTTTATTGTAATG 240  
 Db 203 CCCAACATTTAGTCTTCTTCAATTTCAAGAGAAATGCGAGGCTGTTTATTGTAATG 262  
 QY 241 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACACACGGGGTGTGTTATTT 300  
 Db 263 GAATATTGTGATGGAGGGGATCTCATGAAAAGGATCAATAGACACACGGGGTGTGTTATTT 322  
 QY 301 AGTCAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTTAAACATATTTCAT 360  
 Db 323 AGTCAAGATCAGATCCTCGGTTGGTTTGTACAGATTTCTCTAGGACTTAAACATATTTCAT 382  
 QY 361 GACAGGAAGATATTACACAGGACATAAAAGCTCAGAACATTTTTCTTAGCAAGACGGA 420  
 Db 383 GACAGGAAGATATTACACAGGACATAAAAGCTCAGAACATTTTTCTTAGCAAGACGGA 442  
 QY 421 ATGGTGGCAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTCTGAATTAATTCATGGACTT 480  
 Db 443 ATGGTGGCAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTCTGAATTAATTCATGGACTT 502  
 QY 481 GCTCGAACTTGTATTGGAAACACCTTACTACTCTGCCCCAGAGATCTGTTCAGAAATAAACCC 540  
 Db 503 GCTCGAACTTGTATTGGAAACACCTTACTACTCTGCCCCAGAGATCTGTTCAGAAATAAACCC 562  
 QY 541 TACAAATAAACCGGATATTGGTCTCTTGGCTGTGTCTTATATAGAGCTCTGACACTT 600  
 Db 563 TACAAATAAACCGGATATTGGTCTCTTGGCTGTGTCTTATATAGAGCTCTGACACTT 622  
 QY 601 AACATCTCTTTGAGGGTAAACAACTTACAGCAGCTGGTTCTGAAGATTTCTCAAGACAT 660  
 Db 623 AACATCTCTTTGAGGGTAAACAACTTACAGCAGCTGGTTCTGAAGATTTCTCAAGACAT 682  
 QY 661 TTGCCCCAATATCTCCGGGGTTTCTCGAGAGCTCAATTCCTTGTATATCTAGCTCTTT 720  
 Db 683 TTGCCCCAATATCTCCGGGGTTTCTCGAGAGCTCAATTCCTTGTATATCTAGCTCTTT 742  
 QY 721 CAAATATCTCTCGAGAGCCAGCCATCCATTAATTTCCATTTTGAAGAGGCCCTTTTAGAG 780  
 Db 743 CAAATATCTCTCGAGAGCCAGCCATCCATTAATTTCCATTTTGAAGAGGCCCTTTTAGAG 802  
 QY 781 AATCTTATTTCCCAATATTTTGAATCTCTGAGGCTCATTTCAGGAAGAAATTCAGTCACATGCTT 840  
 Db 803 AATCTTATTTCCCAATATTTTGAATCTCTGAGGCTCATTTCAGGAAGAAATTCAGTCACATGCTT 862  
 QY 841 ATATGAGAGCAGAGGCGCCAGCTTCTCGACATGCTGGGAGAGTGTGTCAGAGAGTGA-A 899  
 Db 863 ATATGAGAGCAGAGGCGCCAGCTTCTCGACATGCTGGGAGAGTGTGTCAGAGAGTGA-ACT 922

QY 900 AATACAAAAGTGAGATCCAGGAAAGTCCACCAAGATCAAGGATATCTGTGCCAAT 959  
 Db 923 GGTGTGAGAGTGGCTCTCAAGGCTTGGGAGCTCTGTCTCTGAGGCTTGGAGGCTA 982  
 QY 960 TAAAGGAATGCTATATATGATAGAAATGAATGGAGACCACCAAGCTGGAGCCCAAGAGGC 1019  
 Db 983 CAGCCCTGGCGCTCTCTCAGG-----CTGCTGTGAGTGTCTGCGGCT 1029  
 QY 1020 CAGATCTATRAAATGATAGAAAGCCCAAAATTTGCTGCTGTGGACATATATGATTA 1079  
 Db 1030 TTTCCAGATAAAATGATAGAAAGCCCAAAATTTGCTGCTGTGGACATATATGATTA 1089  
 QY 1080 TTATTTATGCTCACTTGTATGCTGAGGAGGAGCCCAAAATTTGCTGCTGTGGACATATATGATTA 1139  
 Db 1090 TTATTTATGCTCACTTGTATGCTGAGGAGGAGCCCAAAATTTGCTGCTGTGGACATATATGATTA 1149  
 QY 1140 TCCCTCAAGAAATATGCTGAGTGTAGGATAGGTCAGAAACGAGGATGCTCCATCCC 1199  
 Db 1150 TCCCTCAAGAAATATGCTGAGTGTAGGATAGGTCAGAAACGAGGATGCTCCATCCC 1209  
 QY 1200 AAGTCAATGGCTGCTGAGTACCTTCAAGAAATTTGAAGCTCAAAATATATAGTTGAA 1259  
 Db 1210 AAGTCAATGGCTGCTGAGTACCTTCAAGAAATTTGAAGCTCAAAATATATAGTTGAA 1269  
 QY 1260 AGTGAGAGCAATTTGGTCTTTGCTCCATCTTCTGCCGAGCCAAATTTACAAACAGAGACA 1319  
 Db 1270 AGTGAGAGCAATTT----- 1284  
 QY 1320 AGAGCTAAGAGTAAATGAGAGAGAGCTTAGATTTCCAGGAGTGCCATTTAGGAAACGA 1379  
 Db 1285 ----- 1284  
 QY 1380 AATGAAGCAACAGGAATATTCGAGCAGTTAGAGAAATACGCAACAGTACCAATGA 1439  
 Db 1285 -----GGAATATTCGAGCAGTTAGAGAAATACGCAACAGTACCAATGA 1332  
 QY 1440 CATGAAGCAATTAAGAGAGAGTGGGAGAGAGACCAAGAGAGCACTCAAAATATAGTCA 1499  
 Db 1333 CATGAAGCAATTAAGAGAGAGTGGGAGAGAGACCAAG----- 1370  
 QY 1500 TAAACCTATTTGTTGAAGAGAGTAACTGCTGCTCCATCAAGATGCATCTGAGGAGA 1559  
 Db 1371 ----- 1370  
 QY 1560 AGCAGCTGCGAGGACATTTGAAGAGCTTGAACAAATGAGGCTTCAGAACACAAAGGA 1619  
 Db 1371 -----AGGACATTTGAAGAGCTTGAACAAATGAGGCTTCAGAACACAAAGGA 1419  
 QY 1620 AAGTAAAAATCCAGAACAGAAATATAAGCTAAGAGGGGTAAATTTGAAATTAATTT 1679  
 Db 1420 AAGTAAAAATCCAGAACAGAAATATAAGCTAAGAGGGGTAAATTTGAAATTAATTT 1479  
 QY 1680 AGACAAATGATTTCTGATGAAGAAATCTCTCAAGAGAGAGCAATGATATACCAA 1739  
 Db 1480 AGACAAATGATTTCTGATGAAGAAATCTCTCAAGAGAGAGCAATGATATACCAA 1539  
 QY 1740 TGAACCTTTGACCTTTGAGGATGGCATCAAGTTTAAGAAATATCAATTTGAAAGGAGCA 1799  
 Db 1540 TGAACCTTTGACCTTTGAGGATGGCATCAAGTTTAAGAAATATCAATTTGAAAGGAGCA 1599  
 QY 1800 TGGAGATTATACAGACAAAGCATTTGAAATCTTCACTGCCAGAGAGGGTTTTCCAC 1859  
 Db 1600 TGGAGATTATACAGACAAAGCATTTGAAATCTTCACTGCCAGAGAGGGTTTTCCAC 1659  
 QY 1860 CGAGACTGCTGCTGTTGGAAACAGGAGGAGTGGGATGGAGGCGCTCAGACTCT 1919  
 Db 1660 CGAGACTGCTGCTGTTGGAAACAGGAGGAGTGGGATGGAGGCGCTCAGACTCT 1719  
 QY 1920 GCTGAGATGATGGCAGTGGCGGAGCATCACTCCACCTGCCCCACGGGCGCTGACAGTG 1978  
 Db 1720 GCTGAGATGATGGCAGTGGCGGAGCATCACTCCACCTGCCCCACGGGCGCTGACAGTG 1778

RESULT 9  
 ABX72263  
 ID ABX72263 standard; cDNA; 1597 BP.  
 XX  
 AC ABX72263;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE Human NOVX polynucleotide #94.  
 XX  
 KW Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD;  
 KW hypertension; congenital heart defect; aortic stenosis; valve disease;  
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;  
 KW tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;  
 KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;  
 KW Parkinson's disease; immune disorder; haematopoietic disorder;  
 KW haemophilia; hypercoagulation; Crohn's disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200281498-A2.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 03-APR-2002; 2002WO-US010780.  
 XX  
 PR 03-APR-2001; 2001US-0281086P.  
 PR 03-APR-2001; 2001US-0281136P.  
 PR 05-APR-2001; 2001US-0281863P.  
 PR 05-APR-2001; 2001US-0281908P.  
 PR 06-APR-2001; 2001US-0282020P.  
 PR 10-APR-2001; 2001US-0282930P.  
 PR 10-APR-2001; 2001US-0282934P.  
 PR 12-APR-2001; 2001US-0283512P.  
 PR 13-APR-2001; 2001US-0283710P.  
 PR 17-APR-2001; 2001US-0284234P.  
 PR 19-APR-2001; 2001US-0285325P.  
 PR 20-APR-2001; 2001US-0285381P.  
 PR 20-APR-2001; 2001US-0285609P.  
 PR 23-APR-2001; 2001US-0285748P.  
 PR 23-APR-2001; 2001US-0285890P.  
 PR 24-APR-2001; 2001US-0286068P.  
 PR 25-APR-2001; 2001US-0286292P.  
 PR 27-APR-2001; 2001US-0287213P.  
 PR 02-MAY-2001; 2001US-0288257P.  
 PR 29-MAY-2001; 2001US-0294164P.  
 PR 30-MAY-2001; 2001US-0294484P.  
 PR 18-JUN-2001; 2001US-0298952P.  
 PR 19-JUN-2001; 2001US-0299237P.  
 PR 19-JUN-2001; 2001US-0299276P.  
 PR 12-SEP-2001; 2001US-0318750P.  
 PR 25-SEP-2001; 2001US-0324800P.  
 PR 25-SEP-2001; 2001US-0324802P.  
 PR 27-SEP-2001; 2001US-0325684P.  
 PR 17-OCT-2001; 2001US-0330143P.  
 PR 14-NOV-2001; 2001US-0332131P.  
 PR 14-NOV-2001; 2001US-0332240P.  
 PR 14-NOV-2001; 2001US-0332779P.  
 PR 21-NOV-2001; 2001US-0332115P.  
 PR 04-DEC-2001; 2001US-0337621P.  
 PR 03-JAN-2002; 2002US-0345783P.  
 PR 16-JAN-2002; 2002US-0350251P.  
 PR 02-APR-2002; 2002US-00114270.  
 XX  
 PA (CURA-) CUREGEN CORP.  
 XX  
 PI Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;  
 PI Pattarajan M, Liu X, Gusev V, Li L, Vernet CM, Zehusen BD;  
 PI Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;  
 PI Padigaru M, Shinkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;  
 PI Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;  
 PI Macdougall JR, Rotherberg ME, Mazur A, Millet I, Peyman JA;



PI	Ellerman K;	Db	699	AAACATCCTTTTGGAGGTAAACACTTACAGCAGCTGGTCTGAAGATTTCACAGCACAT	758
XX					
DR	WPI: 2003-046858/04.	Qy	661	TTTGCCCAATATCTCCGGGTTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT	720
DR	P-PSDB; ABU54635.	Db	759	TTTGCCCAATATCTCCGGGTTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT	818
XX					
PT	New isolated NOVX polypeptide useful for treating atherosclerosis,	Qy	721	CAAGTATCTCTCGAGACCCGACCATCCATAAATTCATTTTGAAGGCGCTTTTATAG	780
PT	metabolic disorders, diabetes, obesity, infectious disease, anorexia,	Db	819	CAAGTATCTCTCGAGACCCGACCATCCATAAATTCATTTTGAAGGCGCTTTTATAG	878
XX	neurodegenerative disorders, Alzheimer's disease and cancer.				
XX	Claim 17; Page 291-292; 666pp; English.				
PS					
CC	The invention relates to human polypeptides, termed NOVX, and the	Qy	781	AATCTTATCCCAAAATATTTGACTCTCTGAGGTCA---TTCAGGAAGAATTCAGTCACATG	837
CC	polynucleotides encoding them. The polypeptides and polynucleotides are	Db	879	AATCTTATCCCAAAATATTTGACTCTCTGAGGTCA---TTCAGGAAGAATTCAGTCACATG	938
CC	useful for diagnosing disease, and screening for potential therapeutic				
CC	agents. The sequences are useful for treating metabolic disorders,	Qy	838	CTTATATGCGAGCAGGAGCGCCAGCTTCTCGACATGCTCGGAAGGTGGTCCAGAAAGTGT	897
CC	cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic	Db	939	CTTATATGCGAGCAGGAGCGCCAGCTTCTCGACATGCTCGGAAGGTGGTCCAGAAAGTGT	998
CC	stenosis, atrial septal defect (ASD), atrioventricular canal defect,				
CC	ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular	Qy	898	AAATACAAAAGTGAATTTCCAGGGAAGTGGCCACCAAGATCAAGGATATCTGTGCCA	957
CC	septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,	Db	999	AAATACAAAAGTGAATTTCCAGGGAAGTGGCCACCAAGATCAAGGATATCTGTGCCA	1058
CC	atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative				
CC	disorders, Alzheimer's disease, Parkinson's disease, immune disorders,	Qy	958	ATTAAGGAATGCTATATTTGATATGATGAATGAATGAGACCCAGCTGGAGCCGAGAAG	1017
CC	haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease	Db	1059	ATTAAGGAATGCTATATTTGATATGATGAATGAATGAGACCCAGCTGGAGCCGAGAAG	1118
CC	and cancer. Sequences ABX72170-ABX72275 represent human NOVX				
CC	polynucleotides of the invention				
XX					
SQ	Sequence 1587 BP; 513 A; 313 C; 347 G; 414 T; 0 U; 0 Other;				
	Query Match 58.0%; Score 1190.2; DB 8; Length 1587;				
	Best Local Similarity 99.5%; Pred. No. 0;				
	Matches 1205; Conservative 0; Mismatches 3; Indels 3; Gaps 1;				
Qy	1 ATGGATAGTAGCATGTGATTAAGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	60			
Db	99 ATGGATAGTAGCATGTGATTAAGCCATCGGCAAGTGCCTTCGGGAAGCATACTTA	158			
Qy	61 GCTAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAAGTG	120			
Db	159 GCTAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGAAGTG	218			
Qy	121 CCATACAGAAAAGAGAGCTTCAAGAAAGAGAGTGATCTTCTGGAAAAGATGAACAT	180			
Db	219 CCATACAGAAAAGAGAGCTTCAAGAAAGAGAGTGATCTTCTGGAAAAGATGAACAT	278			
Qy	181 CCCACATTTAGCTCTTCTCAATTCATTTCAAGAGATGCGAGCTCTTTATTTGTAATG	240			
Db	279 CCCACATTTAGCTCTTCTCAATTCATTTCAAGAGATGCGAGCTCTTTATTTGTAATG	338			
Qy	241 GAATATTTGATGGAGGGATCTCATGAAAAGGATCAATAGACACCGGGTGTGTATTT	300			
Db	339 GAATATTTGATGGAGGGATCTCATGAAAAGGATCAATAGACACCGGGTGTGTATTT	398			
Qy	301 AGTGAAGATCAGATCTCGGTGGTTTGTACAGATTTCTTAGACTTAAACATATTTCAT	360			
Db	399 AGTGAAGATCAGATCTCGGTGGTTTGTACAGATTTCTTAGACTTAAACATATTTCAT	458			
Qy	361 GACAGAGAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA	420			
Db	459 GACAGAGAGATATTACACAGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA	518			
Qy	421 ATGGTGGCAAGCTTGGGAGCTTGGTATAGCAAGAGTCTGTAATAATTCATCGAACTT	480			
Db	519 ATGGTGGCAAGCTTGGGAGCTTGGTATAGCAAGAGTCTGTAATAATTCATCGAACTT	578			
Qy	481 GCTCGAATCTGTATTGGAAACACCTTACTACTGCTCCCGAGAGATCTGCAGATATAACCC	540			
Db	579 GCTCGAATCTGTATTGGAAACACCTTACTACTGCTCCCGAGAGATCTGCAGATATAACCC	638			
Qy	541 TACAAATAAAACGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT	600			
Db	639 TACAAATAAAACGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTT	698			
Qy	601 AAACATCTTTTGGGGTAAACACTTACAGCAGCTGGTCTGAAGATTTGTCAAGCACAT	660			

RESULT 10  
ABX72262  
ID ABX72262 standard; cDNA; 1453 BP.

XX AC ABX72262;  
XX AC  
XX AC  
DT 03-JUN-2003 (first entry)  
XX DE Human NOVX polynucleotide #93.

Human; NOVX; Gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; aortic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease; cancer.

OS Homo sapiens.

XX WO200281498-A2.

XX 17-OCT-2002.

PD 03-APR-2002; 2002WO-US010780.

XX 03-APR-2001; 2001US-0281086P.

PR 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281963P.

05-APR-2001; 2001US-0281906P.  
 06-APR-2001; 2001US-0282020P.  
 10-APR-2001; 2001US-0282930P.  
 10-APR-2001; 2001US-0282934P.  
 12-APR-2001; 2001US-0283120P.  
 13-APR-2001; 2001US-0283710P.  
 17-APR-2001; 2001US-0284234P.  
 19-APR-2001; 2001US-0285325P.  
 20-APR-2001; 2001US-0285381P.  
 20-APR-2001; 2001US-0285609P.  
 23-APR-2001; 2001US-0285748P.  
 23-APR-2001; 2001US-0285890P.  
 24-APR-2001; 2001US-0286068P.  
 25-APR-2001; 2001US-0286292P.  
 27-APR-2001; 2001US-0287213P.  
 02-MAY-2001; 2001US-0288257P.  
 29-MAY-2001; 2001US-0294164P.  
 30-MAY-2001; 2001US-0294484P.  
 18-JUN-2001; 2001US-0298952P.  
 19-JUN-2001; 2001US-0299237P.  
 19-JUN-2001; 2001US-0299276P.  
 12-SEP-2001; 2001US-0318750P.  
 25-SEP-2001; 2001US-0324800P.  
 25-SEP-2001; 2001US-0324802P.  
 27-SEP-2001; 2001US-0325684P.  
 17-OCT-2001; 2001US-0330143P.  
 14-NOV-2001; 2001US-0332131P.  
 14-NOV-2001; 2001US-0332240P.  
 14-NOV-2001; 2001US-0332779P.  
 21-NOV-2001; 2001US-0332115P.  
 04-DEC-2001; 2001US-0337621P.  
 03-JAN-2002; 2002US-0345783P.  
 16-JAN-2002; 2002US-0350251P.  
 02-APR-2002; 2002US-00114270.  
 (CURA-) CURAGEN CORP.  
 Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;  
 Patturajan M, Liu X, Gusev VV, Li L, Vernet CAM, Zerhusen BD;  
 Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;  
 Padigar M, Shinkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;  
 Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;  
 MacDougall JR, Rothenberg ME, Mazur A, Millet I, Feyman JA;  
 Ellerman K;  
 WPI; 2003-046858/04.  
 P-PSDB; ABUS4634.  
 New isolated NOVX polypeptide useful for treating atherosclerosis,  
 metabolic disorders, diabetes, obesity, infectious disease, anorexia,  
 neurodegenerative disorders, Alzheimer's disease and cancer.  
 Claim 17; Page 291; 666pp; English.  
 The invention relates to human polypeptides, termed NOVX, and the  
 polynucleotides encoding them. The polypeptides and polynucleotides are  
 useful for diagnosing disease, and screening for potential therapeutic  
 agents. The sequences are useful for treating metabolic disorders,  
 cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic  
 stenosis, atrial septal defect (ASD), atrioventricular canal defect,  
 ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular  
 septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,  
 atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative  
 disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
 haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease  
 and cancer. Sequences ABX72170-ABX72275 represent human NOVX  
 polynucleotides of the invention  
 Query Match 57.4%; Score 1178.4; DB 8; Length 1453;  
 Best Local Similarity 99.2%; Pred. No. 7.6e-312;  
 Matches 1198; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGGTGCTTCGGGAAAGCATACTTA 60  
 DB 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGGTGCTTCGGGAAAGCATACTTA 60  
 QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTTGAAGAATG 120  
 DB 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCTATAAAAGAGATCAATTTTGAAGAAG-- 117  
 QY 121 CCATATAAGAAAGAAAGCTTCAAGAAAGAGTGTCTCTGGAAGAGATGAACAT 180  
 DB 118 -----CAAGAAAGAAAGCTTCAAGAAAGAGTGTCTCTGGAAGAGATGAACAT 171  
 QY 181 CCCAACATTGTAGCCCTTCTCAATTCATTCAAGAGAAATGGCAGGCTGTTTATGTAAATG 240  
 DB 172 CCCAACATTGTAGCCCTTCTCAATTCATTCAAGAGAAATGGCAGGCTGTTTATGTAAATG 231  
 QY 241 GAATATTGTATGAGAGGATCTCATGAAAGGATCAATAGACAACGGGGTGTGTATTT 300  
 DB 232 GAATATTGTATGAGAGGATCTCATGAAAGGATCAATAGACAACGGGGTGTGTATTT 291  
 QY 301 AGTGAAGATCAGATCCTCGGTTGTTCTACAGATTTCTTAGGACTAAAAATATTCAT 360  
 DB 292 AGTGAAGATCAGATCCTCGGTTGTTCTACAGATTTCTTAGGACTAAAAATATTCAT 351  
 QY 361 GACAGGAAGATATTACACAGGAGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420  
 DB 352 GACAGGAAGATATTACACAGGAGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 411  
 QY 421 ATGGTGGCAAGCTTGGGAGCTTGGTATACAGAGAGCTTGAATAATTCATGGAACCT 480  
 DB 412 ATGGTGGCAAGCTTGGGAGCTTGGTATACAGAGAGCTTGAATAATTCATGGAACCT 471  
 QY 481 GCTCGAACTTGTATTGGAAACACCTTACTACCTGTCTCCAGAGATCTGTAGAAATAAACCC 540  
 DB 472 GCTCGAACTTGTATTGGAAACACCTTACTACCTGTCTCCAGAGATCTGTAGAAATAAACCC 531  
 QY 541 TACACAAATAAAAGGATATTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCACACTT 600  
 DB 532 TACACAAATAAAAGGATATTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCACACTT 591  
 QY 601 AAACATCTCTTTGAGGGTAAACACTTACAGAGAGCTGGTTCTGAAGATTTGTCAAGCACAT 660  
 DB 592 AAACATCTCTTTGAGGGTAAACACTTACAGAGAGCTGGTTCTGAAGATTTGTCAAGCACAT 651  
 QY 661 TTTGCCCCAATAATCTCCGGGGTTTCTCGTAGCTCCATTTCTTGATATCTCAGCTCTTT 720  
 DB 652 TTTGCCCCAATAATCTCCGGGGTTTCTCGTAGCTCCATTTCTTGATATCTCAGCTCTTT 711  
 QY 721 CAGATATCTCTCGAGAGCGGACATCCATAATTCATTTGAAAGGCCCTTTTAGAG 780  
 DB 712 CAGATATCTCTCGAGAGCGGACATCCATAATTCATTTGAAAGGCCCTTTTAGAG 771  
 QY 781 AATCTTATTTCCAAATATTGACTCTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTT 840  
 DB 772 AATCTTATTTCCAAATATTGACTCTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTT 831  
 QY 841 ATATGAGAGAGGAGCGGCGGACCTTCTGACATGCTGGAGAGTGTCTCCAGAAGTGTAAA 900  
 DB 832 ATATGAGAGAGGAGCGGCGGACCTTCTGACATGCTGGAGAGTGTCTCCAGAAGTGTAAA 891  
 QY 901 ATACAAAAAGTGAAGATTTCCAGGGAAGTGCACCAAGATCAAGGATATCTGTGCCAATT 960  
 DB 892 ATACAAAAAGTGAAGATTTCCAGGGAAGTGCACCAAGATCAAGGATATCTGTGCCAATT 951  
 QY 961 AAAAGGAATGCTATATTGATAGAAATGAATGAGAACCAAGCTGGAGCCAGAGGCC 1020  
 DB 952 AAAAGGAATGCTATATTGATAGAAATGAATGAGAACCAAGCTGGAGCCAGAGGCC 1011  
 QY 1021 AGATCTTATAAAAAATGATAGAAAGACCCAAAAATTTGCTGTCTGTGGACATTTATGATTAT 1080  
 DB 1012 AGATCTTATAAAAAATGATAGAAAGACCCAAAAATTTGCTGTCTGTGGACATTTATGATTAT 1071

QY 1081 TATTATGCTCAACTGATATGCTGAGGAGAGAGCCCAACCAAGTTATCACCTATT 1140  
 Db |||||  
 1072 TATTATGCTCAACTGATATGCTGAGGAGAGAGCCCAACCAAGTTATCACCTATT 1131  
 QY 1141 CCTCAAGAAATCTGAGGTGAGATACGGTTCAGGAAACGAGGATGCTCATCCCA 1200  
 Db |||||  
 1132 CCTCAAGAAATCTGAGGTGAGATACGGTTCAGGAAACGAGGATGCTCATCCCA 1191  
 QY 1201 AGTCAATG 1208  
 Db |||||  
 1192 AGTCAATG 1199

RESULT 11  
 ABZ77151  
 ID ABZ77151 standard; cDNA; 1632 BP.  
 XX  
 AC ABZ77151;  
 XX  
 DT 07-MAY-2003 (first entry)  
 XX  
 DE Human protein kinase encoding cDNA SEQ ID NO:51.  
 XX  
 KW Human; protein kinase; enzyme; antiasthmatic; antiinflammatory;  
 KW antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic;  
 KW immunosuppressive; vulnary; gene therapy; COPD; asthma; migraine;  
 KW chronic obstructive pulmonary disease; non-insulin dependent diabetes;  
 KW Parkinson's disease; myocardial infarction; inflammatory bowel disease;  
 KW autoimmune disorder; allograft rejection; graft versus host disease;  
 KW cancer; leukaemia; wound granulation; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 CDS 1. .1632  
 FT /tag= a  
 FT /partial  
 FT /product= "protein kinase"  
 FT /note= "no start or stop codons given"  
 XX  
 FN WO2003000901-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 24-JUN-2002; 2002WO-1B002359.  
 XX  
 XX 26-JUN-2001; 2001US-0301098P.  
 PR 06-NOV-2001; 2001US-0332870P.  
 XX  
 PA (DECO-) DECODE GENETICS EHF.  
 XX  
 PI Martinez RAM, Sigurdsson GT;  
 XX  
 DR WPI; 2003-201429/19.  
 DR P-PSDB; ABP96073.  
 XX  
 PT New protein kinase genes and polypeptides, useful for diagnosing diseases  
 PT associated with a protein kinase, or in gene therapy for treating e.g.  
 PT Parkinson's disease, migraine, myocardial infarction, allograft rejection  
 PT or cancers.  
 XX  
 PS Claim 1; Page 76; 258pp; English.  
 XX

CC ABZ77126 to ABZ77165 encode the human protein kinases given in ABP96048  
 CC to ABP96087. The protein kinases have antiasthmatic, antiinflammatory,  
 CC antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic,  
 CC immunosuppressive and vulnary activities, and can be used in gene  
 CC therapy. A protein kinase therapeutic agent from the present invention,  
 CC particularly a protein kinase gene agonist or antagonist, can be used for  
 CC treating a disease or condition associated with a protein kinase in an  
 CC individual. These diseases include chronic obstructive pulmonary diseases  
 CC (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease,  
 CC migraine, myocardial infarction, inflammatory bowel disease, autoimmune

CC disorders (e.g. allograft rejection or graft vs. host disease), cancers  
 CC (e.g. leukaemias) or wound granulation  
 XX  
 SQ Sequence 1632 BP; 459 A; 354 C; 415 G; 404 T; 0 U; 0 Other;  
 Query Match 29.3%; Score 602; DB 10; Length 1632;  
 Best Local Similarity 98.4%; Pred. No. 6.3e-154;  
 Matches 508; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 204 TTCATTTCAAGAAATGCGAGCTGTTTATTGTAATGGAATATTGTGATGAGGGGATCT 263  
 Db |||||  
 201 TTTCTTACAGAGAAATGCGAGCTGTTTATTGTAATGGAATATTGTGATGAGGGGATCT 260  
 QY 264 CATGAAAAGGATCAATAGACACCGGGTGTGTTATTAGTCAAGATCAGATCCCTCGGTG 323  
 Db |||||  
 261 CATGAAAAGGATCAATAGACACCGGGTGTGTTATTAGTCAAGATCAGATCCCTCGGTG 320  
 QY 324 GTTTGTACAGATTTCTCTAGSACTAAACATATTTCATGACAGGAAGATATTACACAGGA 383  
 Db |||||  
 321 GTTTGTACAGATTTCTCTAGSACTAAACATATTTCATGACAGGAAGATATTACACAGGA 380  
 QY 384 CATRAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGTTGCAAAAGCTTGGGACTT 443  
 Db |||||  
 381 CATRAAGCTCAGAACATTTTCTTAGCAAGAACGGAATGTTGCAAAAGCTTGGGACTT 440  
 QY 444 TGGTATAGCAAGAGTCTCTGAATTAATTCATGGAACCTTGTCTCGAATTTGTAATGGAAACACC 503  
 Db |||||  
 441 TGGTATAGCAAGAGTCTCTGAATTAATTCATGGAACCTTGTCTCGAATTTGTAATGGAAACACC 500  
 QY 504 TTACTACTGTCCCGCAGAGATCTGTGAGATAAACCTTCAAGACACATTTTGCCTCGACCGATATTG 563  
 Db |||||  
 501 TTACTACTGTCCCGCAGAGATCTGTGAGATAAACCTTCAAGACACATTTTGCCTCGACCGATATTG 560  
 QY 564 GTCTCTTGGGTGTGTTTATATGAGCTCTGACACTTAAACATCTTTTTCGAGGTAACAA 623  
 Db |||||  
 561 GTCTCTTGGGTGTGTTTATATGAGCTCTGACACTTAAACATCTTTTTCGAGGTAACAA 620  
 QY 624 CTTACAGAGCTGGTCTGAAGATTGTGCAAGACATTTTGCCTCGACCGATATTGCTCCGGGGTT 683  
 Db |||||  
 621 CTTACAGAGCTGGTCTGAAGATTGTGCAAGACATTTTGCCTCGACCGATATTGCTCCGGGGTT 680  
 QY 684 TTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTCAAGTATCTCTCGACCGACACC 743  
 Db |||||  
 681 TTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTCAAGTATCTCTCGACCGACACC 740  
 QY 744 ATCCATAAATTCATTTTGAAGAGCCCTTTTAGAGAAATCTTTATCCCAAAATATTGAC 803  
 Db |||||  
 741 ATCCATAAATTCATTTTGAAGAGCCCTTTTAGAGAAATCTTTATCCCAAAATATTGAC 800  
 QY 804 TCCTGAGGTCAATTCAGGA 821  
 Db |||||  
 801 TCCTGAGGTAAAGTTTGA 818

RESULT 12  
 ADF44502  
 ID ADF44502 standard; cDNA; 1434 BP.  
 XX  
 AC ADF44502;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Mouse kinase protein encoding cDNA SEQ ID NO:20.  
 XX  
 KW cytostatic; nootropic; neuroprotective; antidiabetic; screening;  
 KW regulation; drug development; protein-associated disease; cancer;  
 KW dementia; diabetes; kinase; enzyme; mouse; gene; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003084992-A1.  
 XX  
 PD 16-OCT-2003.

XX PF 04-APR-2003; 2003WO-JP004330.  
 XX PR 05-APR-2002; 2002JP-00103396.  
 XX PR 23-APR-2002; 2002JP-00120904.  
 XX PR 02-MAY-2002; 2002JP-00130601.  
 XX PR 04-DEC-2002; 2002JP-00352520.  
 XX (RIKE) RIKEN KK.  
 XX PA (DNAP-) DNAPFORM KK.  
 XX PA (MITU) MITSUBISHI CHEM CORP.  
 XX PI Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;  
 XX WPI; 2003-833568/77.  
 XX DR P-PSDB; ADF44528.  
 XX PT Proteins and encoded DNAs with kinase activity, useful in screening  
 XX PT substances for regulating such activity and in developing drugs for the  
 XX PT protein-associated diseases e.g. cancer, dementia and diabetes.  
 XX PS Claim 4; SEQ ID NO 20; 342pp; Japanese.  
 CC The present invention describes a protein: (a) containing any of the  
 CC amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on  
 CC any of the sequences in (a) but with some amino acids deleted,  
 CC substituted and/or added and having kinase activity. Also described: (1)  
 CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the  
 CC protein; (3) a DNA which is: (a) a DNA containing any of the base  
 CC sequences in ADF44483 to ADF44508 or ADF44543; (b) a DNA derived from any  
 CC of the sequences in (a) but with some bases deleted, substituted and/or  
 CC added and encoding a protein with kinase activity; or (c) a DNA  
 CC hybridizable with any of the sequences in (a) or their complementary  
 CC strands under stringent conditions and encoding a protein with kinase  
 CC activity; (4) a recombinant vector containing the DNA; (5) a cell  
 CC transfected with the DNA or recombinant vector, or an individual produced  
 CC from the cell; (6) recombinant proteins produced by such cells; (7) an  
 CC oligonucleotide containing 5-10 consecutive bases in any of the base  
 CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a  
 CC complementary strand of such sense oligonucleotide, or an oligonucleotide  
 CC derivative of the (anti-)sense oligonucleotide; (8) an antibody  
 CC specifically binding to the protein, or its partial fragment; (9) a  
 CC method for screening substances for regulating activity of the protein by  
 CC contacting a test substance with such protein before measuring changes in  
 CC the protein activity due to the test substance; (10) a method for  
 CC screening substances regulating expression of the DNA by contacting a  
 CC test substance with cells transfected with the gene and detecting changes  
 CC in expression level of the DNA in such cells; (11) recordable media for  
 CC reading in a computer with information on the amino acid sequences of the  
 CC proteins, and/or base sequences of the DNAs stored; and (12) a support  
 CC for binding with any of the proteins and/or DNAs. The proteins and their  
 CC encoded DNAs have cytostatic, neurotropic, neuroprotective and antidiabetic  
 CC activities. They can be used in screening substances for regulating such  
 CC activity and in developing drugs for the protein-associated diseases e.g.  
 CC cancer, dementia and diabetes. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX SQ Sequence 1434 BP; 392 A; 338 C; 336 G; 368 T; 0 U; 0 Other;  
 Query Match 29.0%; Score 595.4; DB 10; Length 1434;  
 Best Local Similarity 80.3%; Pred. No. 3.8e-152;  
 Matches 728; Conservative 0; Mismatches 166; Indels 13; Gaps 2;  
 1 ATGGTAAGTACGATGTAATGAAGCCATCGGGAGGCTGCTCCGGAAGCATCTTA 60  
 104 ATGGTAAGTACGATGTAATGAAGCCATCGGGAGGCTGCTCCGGAAGCATCTTA 163  
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 QY 361 GACAGGAGATATTACAGAGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420  
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 Db 512 ATGGTTGCCAGCTCGGGACTTTTGAACACAGCAAGACACTGAATGACTTCCATGGAATTT 571  
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 Db 572 GCTCAACATGTTGGGACACCTTACTACCTGTCCTCCAGAGATCTGTCAAGACAGGCA 631  
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 QY 721 CAAGTATCTCTGAGACCGGACATCCATTAATTCATTTGAAAGGCCCTTTTAGAG 780  
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 QY 840 TATATCAGAGCAGGAGCGGACCTTCTGACATGCTGGGAAAGGTGTCAGAAAGTGTAA 899  
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 DE Mouse kinase protein encoding cDNA SEQ ID NO:7.  
 XX  
 XX cytostatic; neurotropic; neuroprotective; antidiabetic; screening;  
 XX regulation; drug development; protein-associated disease; cancer;  
 XX dementia; diabetes; kinase; enzyme; mouse; gene; ss.  
 XX Mus musculus.  
 XX  
 XX WO2003084992-A1.  
 XX



XX PD 23-AUG-2001.  
 XX PF 15-FEB-2001; 2001WO-US005356.  
 XX PR 18-FEB-2000; 2000US-0183582P.  
 XX PR 22-FEB-2000; 2000US-0184014P.  
 XX PA (LEXI-) LEXICON GENETICS INC.  
 XX PI Walke DW, Hu Y, Nepomnichy B, Turner CA, Zambrowicz B;  
 XX DR WPI; 2001-502793/55.  
 XX DR P-PSDB; AAU07102.  
 XX PT Isolated nucleic acids encoding novel human proteins useful for the  
 XX PT treatment of disease and as probes for testing and detection.  
 XX PS Disclosure; Page 35-37; 69pp; English.  
 XX CC The invention relates to novel human proteins (NHP) and the nucleic acids  
 XX CC encoding them. The nucleic acids encode mammalian transporter proteins  
 XX CC and are useful for the treatment (e.g. by gene therapy or antisense  
 XX CC technology) of any of a wide variety of symptoms associated with  
 XX CC biological disorders (e.g. breast and prostate cancer) or imbalances and  
 XX CC as probes for the identification, selection and validation of novel  
 XX CC molecular targets for drug discovery. The proteins may be used to raise  
 XX CC anti-NHP antibodies. The present sequence encodes an NHP of the invention  
 XX SQ Sequence 3645 BP; 1327 A; 594 C; 822 G; 902 T; 0 U; 0 Other;  
 Query Match 17.9%; Score 368; DB 5; Length 3645;  
 Best Local Similarity 66.0%; Pred. No. 1.2e-89;  
 Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;  
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 DB 1 ATGGAGAAGTATGTTAGACTACAGAGATGAGAGGTTTCATTGGAAAGCCATTCTT 60  
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 QY 481 GCTCGAATCTGATTGGAAACATCTTACTACCTGTCGCCAGAGATCTGTGAGAATAAACC 540  
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DB 538 TACAATAATAAAGTGACATTTGGGCTCTGGGGTGTGCTCTTTATGAGTGTACACTT 597  
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 QY 661 TTGCCCCAATATCTCCGGGGTTTCTCTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
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 ID AAL51590 standard; DNA; 3729 BP.  
 XX AC AAL51590;  
 XX DT 10-APR-2003 (first entry)  
 XX DE Human serine/threonine protein kinase NEK1 coding sequence #1.  
 XX KW Human; gene; ds; gene therapy; serine/threonine protein kinase; NEK1;  
 KW cancer; colon cancer; cardiovascular disorder; congestive heart failure;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;  
 KW CNS disorder; diabetes; myocardial infarction; ischaemic heart disease;  
 KW arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease;  
 KW peripheral pain; chronic pain.  
 XX OS Homo sapiens.  
 XX FH Key  
 FT CDS  
 FT 1..3729  
 FT /\*tag= a  
 FT /product= "Human serine/threonine protein kinase NEK1"  
 XX PN WO2003000873-A2.  
 XX PD 03-JAN-2003.  
 XX PF 21-JUN-2002; 2002WO-BP006879.  
 XX PR 25-JUN-2001; 2001US-0300071P.  
 XX PR 18-NOV-2001; 2001US-0331447P.  
 XX PR 07-DEC-2001; 2001US-0336693P.  
 XX PA (FARB ) BAYER AG.  
 XX PI Xiao Y;  
 XX DR WPI; 2003-201424/19.  
 XX DR P-PSDB; AAO16440.  
 XX PT New serine/threonine protein kinase NEK1 gene and protein, useful for  
 XX PT identifying modulators of serine/threonine protein kinase NEK1 activity,  
 XX PT and in gene therapy for treating cancer, diabetes, heart failure or  
 XX PT Alzheimer's disease.  
 XX PS Claim 1; Fig 1; 156pp; English.  
 XX CC The invention comprises the amino acid and coding sequence of the human  
 XX CC serine/threonine protein kinase NEK1. The DNA and protein sequences of  
 XX CC the invention are useful for modulating the activity of serine/threonine  
 XX CC kinase NEK1 in a disease, such as: cancer (particularly colon cancer);  
 XX CC cardiovascular disorders; central nervous system (CNS) disorders;  
 XX CC diabetes; and chronic obstructive pulmonary disease. In particular the

CC DNA and protein sequences of the invention are useful for treating:  
CC congestive heart failure; myocardial infarction; ischaemic heart disease;  
CC arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease; and  
CC peripheral or chronic pain. The present DNA sequence encodes the human  
CC serine/threonine protein kinase NEX1 of the invention  
XX  
SQ Sequence 3729 BP; 1358 A; 611 C; 849 G; 911 T; 0 U; 0 Other;

Query Match 17.9%; Score 368; DB 8; Length 3729;  
Best Local Similarity 66.0%; Pred. No. 1.2e-89;  
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGSCAAGGTGCCTTCGGGAAAGCATACTTA 60  
DB |||||  
QY 1 ATGCGAAGTATGTTAGACTACAGAAGATGGAGAAGTTCATTTGGAAAGCCATCTT 60  
DB |||||  
QY 61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCATATAAAGAGATCAATTTGAAAGATG 120  
DB |||||  
QY 61 GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAGGAAATTAACATCTCAAGATG 120  
DB |||||  
QY 121 CCCATACAGAAAGAGCTTCAAGAAAGAGTGTCTTCTGGAAGATGAACAT 180  
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QY 121 TCCAGTAAAGAAAGAGAAATCAAGGAGAGAGTTCAGATATTGGCAACATGAAGCAT 180  
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QY 181 CCCAATCTGTACCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGTTATTGTAATG 240  
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QY 421 ACAGT---ACACTTGGAGATTTTGAATTTGTAAGTCTAGAGTTCCTTAATAGTACTGAGGCTG 477  
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QY 478 GCTCGAATCTGCATAGGACCCCATACTACTTGTCACTGAAATCTGTGANAACAACT 537  
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QY 541 TACAACAATAAAGCGATATTTGGTCTCTTGGCTGTCTTATATGAGCTCTGCACACTT 600  
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QY 598 AAACATGCTTTTGAAGCTGGCAGTATGAATAACCTGGTACTGAAGATATATCTGGATCT 657  
DB |||||  
QY 661 TTGCCCCAATATCTCCGGGGTTTCTCGTGAAGTCCATTCCTGATATCTCAGCTCTTT 720  
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QY 658 TTTCACCTGTGTCTTGGCATTTCCATATGATCTCCGAGTTTGGTGTCTCAGTTATT 717  
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QY 721 CAAGTATCTCCGAGACCGACCCATCCATAAATTCATTTGAAAGGCCCTTTTAGAG 780  
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QY 718 AAAGAAATCTTAGGATAGACCATCAGTCAACTCCATATTGGAGAAAGGTTTTATAGCC 777  
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QY 781 AATCTTATTTCCAAATATTGACTCCTGAGGTCAATTGAGGAAGAAATTCAGTC 832  
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QY 778 AAAGCATTTGAAAAGTTTCTCTCTCTCAGCTTATTGCAAGAGAAATTTTGC 829  
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Search completed: October 10, 2004, 04:52:56  
Job time : 1438 secs





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		Match	Length		
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3	1868	91.0	1965	9	US-09-940-921B-3
4	1654	80.6	2370	14	US-10-243-735-1
5	1654	80.6	2370	17	US-10-730-010-1
6	1190.2	58.0	1587	16	US-10-114-270-187
7	1178.4	57.4	1453	16	US-10-114-270-185
8	368	17.9	3645	9	US-09-783-320-3
9	368	17.9	5426	9	US-09-783-320-50
10	368	17.9	5448	15	US-10-037-270-246
11	368	17.9	5448	15	US-10-117-722-246
12	368	17.9	5532	15	US-10-037-270-245
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十一

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RESULT 2

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 ; Patent No. US20020147320A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Friddle, Carl Johan  
 ; APPLICANT: Hilbun, Erin  
 ; APPLICANT: Nepomnichy, Boris  
 ; APPLICANT: Hu, Yi  
 ; TITLE OF INVENTION: No. US20020147320A1 Human Kinase Proteins and Polynucleotides  
 ; FILE REFERENCE: LEX-0227-USA  
 ; CURRENT FILING DATE: 2002-05-21  
 ; PRIOR APPLICATION NUMBER: US 60/229,289

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; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
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QY 781 AATCTTATTTCCCAATATTTGACTCTGAGGTCATTCAGGAAGATTCAGTCACATGCTT 840
DB 885 AATCTTATTTCCCAATATTTGACTCTGAGGTCATTCAGGAAGATTCAGTCACATGCTT 944

QY 841 ATATGACAGACGAGGCGGACCTTCTCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 900
DB 945 ATATGACAGACGAGGCGGACCTTCTCGACATGCTGGGAAGTGGTCCAGAAGTGTAAA 1004
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QY 901 ATACAAAAGTGAATTCAGGGAAAGTGCCCAAGATCAAGATATCTGTCCCAATT 960
DB 1005 ATACAAAAGTGAATTCAGGGAAAGTGCCCAAGATCAAGATATCTGTCCCAATT 1064

QY 961 AAAAGGAATGCTATATTGCTATAGAAATGAATGAGACCAACAGCTGAGGCCAGAGGCC 1020
DB 1065 AAAAGGAATGCTATATTGCTATAGAAATGAATGAGACCAACAGCTGAGGCCAGAGGCC 1124

QY 1021 AGATCTATAAAAATGATAGAAAAGCCCAAAATTTGCTCTGTCTGTGACATTTATGATTAT 1080
DB 1125 AGATCTATAAAAATGATAGAAAAGCCCAAAATTTGCTCTGTCTGTGACATTTATGATTAT 1184

QY 1081 TATTATGCTCAACTGATGATGCTGAGGAGGAGCCCAAAAACCAAGTTATCAACCTTATT 1140
DB 1185 TATTATGCTCAACTGATGATGCTGAGGAGGAGCCCAAAAACCAAGTTATCAACCTTATT 1244

QY 1141 CCTCAAGAAATACCTGAGTTGAGGATTACGGTCAGAAACGAGGATGTCATCCCCA 1200
DB 1245 CCTCAAGAAATACCTGAGTTGAGGATTACGGTCAGAAACGAGGATGTCATCCCCA 1304

QY 1201 AGTCAATGGCTGCTGAGTACCTTTCAGAGAAAATTTTGAAGCTCAACAAATATAAGTTGAAA 1260
DB 1305 AGTCAATGGCTGCTGAGTACCTTTCAGAGAAAATTTTGAAGCTCAACAAATATAAGTTGAAA 1364

QY 1261 GTGAGAGAACTATGGGCTCTTCGTCATCTTCTGCCGAGCCAAATTAACACGAGACAA 1320
DB 1365 GTGAGAGAACTATGGGCTCTTCGTCATCTTCTGCCGAGCCAAATTAACACGAGACAA 1424

QY 1321 GAGCTAAGAAATTAAGTGAAGAGAGCTTAGATTCCAGAGAGCTGCCATTTAGGAAAAACGAA 1380
DB 1425 GAGCTAAGAAATTAAGTGAAGAGAGCTTAGATTCCAGAGAGCTGCCATTTAGGAAAAACGAA 1484

QY 1381 ATGAAGAAACAGGAAATTTGGAAGCAGTTAGAGAAATACGCCAACAGTACCAATGAC 1440
DB 1485 ATGAAGAAACAGGAAATTTGGAAGCAGTTAGAGAAATACGCCAACAGTACCAATGAC 1544

QY 1441 ATGAAGAAATTAAGAAAGAGATGGGAGAGAAACAGAGAGAGAACTCAAAAATAAGTCAT 1500
DB 1545 ATGAAGAAATTAAGAAAGAGATGGGAGAGAAACAGAGAGAGAACTCAAAAATAAGTCAT 1604

QY 1501 AAAACCTATTGTGTAAGAAAGATPAACCTGCTGTCCATCAAGATGCTATGAGGGAGAA 1560
DB 1605 AAAACCTATTGTGTAAGAAAGATPAACCTGCTGTCCATCAAGATGCTATGAGGGAGAA 1664

QY 1561 GCACCTGTGAGGACATTTGAAGAGCTTGAACAAATGAGGCTTCAGACACAAAGGAA 1620
DB 1665 GCACCTGTGAGGACATTTGAAGAGCTTGAACAAATGAGGCTTCAGACACAAAGGAA 1724

QY 1621 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAAAGGGGTAAAAATTTGAAATTAATTTA 1680
DB 1725 AGTAAAAATCCAGAACAGAAATATAAAGCTAAGAAAGGGGTAAAAATTTGAAATTAATTTA 1784

QY 1681 GACAAATGTTATTTGATGAAACATCTCTCAAGAGAGAGGCAATGGATATACCAAT 1740
DB 1785 GACAAATGTTATTTGATGAAACATCTCTCAAGAGAGAGGCAATGGATATACCAAT 1844

QY 1741 GAAACTTTGACCTTTGAGGATGCTGAAGTTTAAAGAAATATGAATGTTAAAGAGAGCAT 1800
DB 1845 GAAACTTTGACCTTTGAGGATGCTGAAGTTTAAAGAAATATGAATGTTAAAGAGAGCAT 1904

QY 1801 GGAGATTATACAGACAAAGCATTTGAAAAAATCTCACTGCCAGAGAGCGGTTTTTCACG 1860
DB 1905 GGAGATTATACAGACAAAGCATTTGAAAAAATCTCACTGCCAGAGAGCGGTTTTTCACG 1964

QY 1861 CAGACTGTAGCTGTGGGAAACAGGAGGAGTGGATGGAGGAGCGCTCAGACTCTG 1920
DB 1965 CAGACTGTAGCTGTGGGAAACAGGAGGAGTGGATGGAGGAGCGCTCAGACTCTG 2024

QY 1921 CTGAGATGATGGCAGTGGCCGACATCACTCCACTGCCCCACGGGCGCTGACGTGAG 1980
DB 2025 CTGAGATGATGGCAGTGGCCGACATCACTCCACTGCCCCACGGGCGCTGACGTGAG 2084

QY 1981 TCTGTCTTAGCTCAGTCTGTGAGGAAGGGAAGCAAGACCCGTACAGCCCGAGTCTC 2040
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Db      2085 TCTGTGCTTAGCGTCAGTGTGAGGAGGAGCAAGGACCCGTCAGAGCCGAGTGTCT 2144
Qy      2041 ATCCTGATGTGA 2052
Db      2145 ATCCTGATGTGA 2156

RESULT 3
US-09-940-921B-3
; Sequence 3, Application US/09940921B
; Patent No. US20020147320A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: No. US20020147320A1el Human Kinase Proteins and Polynucleotides
; FILE REFERENCE: LEX-0227-USA
; CURRENT APPLICATION NUMBER: US/09/940,921B
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/229,280
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-940-921B-3

Query Match          91.0%; Score 1868; DB 9; Length 1965;
Best Local Similarity 95.8%; Pred No. 0;
Matches 1965; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

Qy      1  ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGTGCCTTCGGAAAGCATCTTA 60
Db      1  ATGGATAAGTACGATGTGATTAAAGCCATCGGGCAAGTGCCTTCGGAAAGCATCTTA 60

Qy      61  GCTAAGGGAATCAGATAGCAGCACTGTCTATAAAGAGATCAATTTTGAAGAATG 120
Db      61  GCTAAGGGAATCAGATAGCAGCACTGTCTATAAAGAGATCAATTTTGAAGAATG 120

Qy      121  CCATACAGAAAGAAAGAGCTTCAAGAAAGAGATGATTTCTTGGAAAGATGAACAT 180
Db      121  CCATACAGAAAGAAAGAGCTTCAAGAAAGAGATGATTTCTTGGAAAGATGAACAT 180

Qy      181  CCCAATATGTAGCTTCTTCAATTCATTTCAAGAGATGCGAGGCTGTTTATGTAATG 240
Db      181  CCCAATATGTAGCTTCTTCAATTCATTTCAAGAGATGCGAGGCTGTTTATGTAATG 240

Qy      241  GAATATGTGATGAGGGGATCTCATGAAAGAGATCAATAGCAACGGGGTGTGTTATTT 300
Db      241  GAATATGTGATGAGGGGATCTCATGAAAGAGATCAATAGCAACGGGGTGTGTTATTT 300

Qy      301  AGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCTTAGACTTAACATATTTCAT 360
Db      301  AGTGAAGATCAGATCCTCGGTGGTTGTACAGATTTCTTAGACTTAACATATTTCAT 360

Qy      361  GACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 420
Db      361  GACAGGAAGATATTACAGGGACATAAAGCTCAGAACATTTTCTTAGCAAGACGGA 420

Qy      421  ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGATCTTCAATATTCATGAACTT 480
Db      421  ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGATCTTCAATATTCATGAACTT 480

Qy      481  GCTCGAATCTGTTATGGAACACCTTACTACCTGTCGCCAGAGATCTGTCAAGTAACCC 540
Db      481  GCTCGAATCTGTTATGGAACACCTTACTACCTGTCGCCAGAGATCTGTCAAGTAACCC 540

Qy      541  TACAAACAATAAAGGATATTGGTCTCTTGGCTGTGTTTATATGAGCTCTGCACACTT 600

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Db      541  TACAAACAATAAAGGATATTGGTCTCTTGGCTGTGTTTATATGAGCTCTGCACACTT 600
Qy      601  AAACATCTCTTTTGGAGGTAAACAACTTACAGCAGCTGGTTCTTGAAGATTTTGTCAAGCACAT 660
Db      601  AAACATCTCTTTTGGAGGTAAACAACTTACAGCAGCTGGTTCTTGAAGATTTTGTCAAGCACAT 660
Qy      661  TTTGCCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT 720
Db      661  TTTGCCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGATATCTCAGCTCTTT 720
Qy      721  CAAAGTATCTCTCGAGACCGACCATCAATAATTTGAAAGAGGCCCCCTTTTAGAG 780
Db      721  CAAAGTATCTCTCGAGACCGACCATCAATAATTTGAAAGAGGCCCCCTTTTAGAG 780
Qy      781  AATCTTATTTCCCAATATTGTAATCTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTT 840
Db      781  AATCTTATTTCCCAATATTGTAATCTCTGAGGTCAATTCAGGAAGAAATTCAGTCAATGCTT 840
Qy      841  ATATGAGAGCAGGAGCGCCAGCTTCTGCACATGCTGGGAAGTGGTCCAGAAAGTGTAAA 900
Db      841  ATATGAGAGCAGGAGCGCCAGCTTCTGCACATGCTGGGAAGTGGTCCAGAAAGTGTAAA 900
Qy      901  ATACAAAAAGTGAATTCAGGAAAGTCCCAAGATCAAGGATATCTGTGCAATTT 960
Db      901  ATACAAAAAGTGAATTCAGGAAAGTCCCAAGATCAAGGATATCTGTGCAATTT 960
Qy      961  AAAAGGAATGCTATATTGATAGAAATGAATGAGACCAAGCTGGAGCCAGAGGCC 1020
Db      961  AAAAGGAATGCTATATTGATAGAAATGAATGAGACCAAGCTGGAGCCAGAGGCC 1020
Qy      1021  AGATCTATAAAAAATGATAGAAAGACCCAAAATTTGCTGTCTGTGGAATATGATTTAT 1080
Db      1021  AGATCTATAAAAAATGATAGAAAGACCCAAAATTTGCTGTCTGTGGAATATGATTTAT 1080
Qy      1081  TATTATGCTCAACTTGATATGCTGAGGAGAGGCCCAACCAAGTATCACCTTAT 1140
Db      1081  TATTATGCTCAACTTGATATGCTGAGGAGAGGCCCAACCAAGTATCACCTTAT 1140
Qy      1141  CCTCAAGAAAAATACCTGAGGTGAGGATACGGTACAGGAAACGAGGATGCTGTCATCCCA 1200
Db      1141  CCTCAAGAAAAATACCTGAGGTGAGGATACGGTACAGGAAACGAGGATGCTGTCATCCCA 1200
Qy      1201  AGTCAATGCGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACATATAAGTTGAAA 1260
Db      1201  AGTCAATGCGCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACATATAAGTTGAAA 1260
Qy      1261  GTGGAGAACAATTTGGTCTTCTGTCCTCCTGCGAGCCAAATTCACACAGAGACAA 1320
Db      1261  GTGGAGAACAATTTGGTCTTCTGTCCTCCTGCGAGCCAAATTCACACAGAGACAA 1320
Qy      1321  GAGCTAAGAAGTAATGGAGAAGAGCTAGATTCAGAGAGTCCCATTTAGGAAAAACGAA 1380
Db      1321  GAGCTAAGAAGTAATGGAGAAGAGCTAGATTCAGAGAGTCCCATTTAGGAAAAACGAA 1380
Qy      1381  ATGAGGAACAGGAATATTGGAAGCAGTTAGAGGAAATACGCCAACAGTACCAATGAC 1440
Db      1381  ATGAGGAAC----- 1390
Qy      1441  ATGAAAGAAATTAGAAGAGATGGGAGAGAACCCAGAGGAGAACTCAAAAAATAGTCAT 1500
Db      1391  -----AGGAGAACTCAAAAAATAGTCAT 1413
Qy      1501  AAAACCTATTGGTGAAGAGAGTAACCTGCTGTCATCAAGATGCAATCTGAGGAGAA 1560
Db      1414  AAAACCTATTGGTGAAGAGAGTAACCTGCTGTCATCAAGATGCAATCTGAGGAGAA 1473
Qy      1561  GCACCTGTGAGGACATTTGAAAAAGCTTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1620
Db      1474  GCACCTGTGAGGACATTTGAAAAAGCTTTGAAACAAATGAGGCTTCAGAACACAAAGGAA 1533
Qy      1621  AGTAAAAATCCAGAGACAGAAATATTAAGCTAAGAGAGGGGGTAAAAATTTGAAATTAATTTA 1680
Db      1534  AGTAAAAATCCAGAGACAGAAATATTAAGCTAAGAGAGGGGGTAAAAATTTGAAATTAATTTA 1593

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QY 1381 ATGAAGAACAGGAATATTGGAGCAGTTAGAGGAATAACGCCAACAGTACCAATGAC 1440
Db 1392 ATGAAGAACAGGAATATTGGAGCAGTTAGAGGAATAACGCCAACAGTACCAATGAC 1451
QY 1441 ATGAAGAACAGGAATATTGGAGCAGTTAGAGGAATAACGCCAACAGTACCAATGAC 1500
Db 1452 ATGAAGAACAGGAATATTGGAGCAGTTAGAGGAATAACGCCAACAGTACCAATGAC 1488
QY 1501 AAAACCTATTGCTGAAGAGAGTAACCTGCTGCTCAATCAAGATGCAATCTGAGGGAGAA 1560
Db 1489 ----- 1488
QY 1561 GCACCTGTGCAGGACATTTGAAAAGACTTGAACAAATGAGCTTCAGAACACAAAGGAA 1620
Db 1489 -----AGGACATTTGAAGAGACTTTGAACAAATGAGCTTCAGAACACAAAGGAA 1538
QY 1621 AGTAAATCCAGAACAGGAATATAAGCTTAAGAGGGGGTAAATTTGAAATTAATTA 1680
Db 1539 AGTAAATCCAGAACAGGAATATAAGCTTAAGAGGGGGTAAATTTGAAATTAATTA 1598
QY 1681 GACAAATGATTTCTGATGAAGAACATCTCCAGAGGAGAGGCAATGATATACCAAT 1740
Db 1599 GACAAATGATTTCTGATGAAGAACATCTCCAGAGGAGAGGCAATGATATACCAAT 1658
QY 1741 GAAACTTTGACCTTTGAGATGGCATGAAGTTTAAGGAATATGAATGTGTAAGGAGCAT 1800
Db 1659 GAAACTTTGACCTTTGAGATGGCATGAAGTTTAAGGAATATGAATGTGTAAGGAGCAT 1718
QY 1801 GGAGATTATACAGACAAAGCATTTGAAAACCTTCACTGCCAGAGAGGGTTTCCACG 1860
Db 1719 GGAGATTATACAGACAAAGCATTTGAAAACCTTCACTGCCAGAGAGGCAATTTACAGAA 1778
QY 1861 CAGACT 1866
Db 1779 CTGACT 1784

RESULT 5
US-10-730-010-1
; Sequence 1, Application US/10730010
; Publication No. US20040142366A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212CIPDIV-II
; CURRENT APPLICATION NUMBER: US/10/730,010
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-730-010-1

Query Match 80.6%; Score 1654; DB 17; Length 2370;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 10; Indels 93; Gaps 1;

QY 1 ATGGATAAGTACGATGATTAAGGCCATCGGCAAGGTGCTTCGGGAAGAGCATCTTA 60
Db 12 ATGGATAAGTACGATGATTAAGGCCATCGGCAAGGTGCTTCGGGAAGAGCATCTTA 71
QY 61 GCTAAAGGAAATACATAGATAGCAAGCATGTGTCATAAAGAGATCAATTTGAAAGATG 120
Db 72 GCTAAAGGAAATACATAGATAGCAAGCATGTGTCATAAAGAGATCAATTTGAAAGATG 131
QY 121 CCCATACAGAAAGAGAGCTTCAAGAGAAAGATGATTTCTTGGAAAGATGAAACAT 180
Db 132 CCCATACAGAAAGAGAGCTTCAAGAGAAAGATGATTTCTTGGAAAGATGAAACAT 191
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QY 181 CCCAATTTGTAGCTTCTCAATTCATTTCAAGAGATGGCAGGCTGTTTATTGTAATG 240
Db 192 CCCAATTTGTAGCTTCTCAATTCATTTCAAGAGATGGCAGGCTGTTTATTGTAATG 251
QY 241 GAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATT 300
Db 252 GAATATTGTGATGGAGGGATCTCATGAAAAGGATCAATAGACAACGGGGTGTGTTATT 311
QY 301 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTAGGACTAAAACATATTAT 360
Db 312 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTAGGACTAAAACATATTAT 371
QY 361 GACAGGAAGATATTACAGAGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 420
Db 372 GACAGGAAGATATTACAGAGGACATAAAAGCTCAGAACATTTTCTTAGCAAGAACGGA 431
QY 421 ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGTCTCGAATAATTCATGGAATCT 480
Db 432 ATGGTGGCAAGCTTGGGACCTTTGGTATAGCAAGAGTCTCGAATAATTCATGGAATCT 491
QY 481 GCTCGAATCTTGTATTGGAACACCTTACTACCTGCCCCAGAGATCTGTGAGATTAACCC 540
Db 492 GCTCGAATCTTGTATTGGAACACCTTACTACCTGCCCCAGAGATCTGTGAGATTAACCC 551
QY 541 TACAACAATAAAACGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACATCT 600
Db 552 TACAACAATAAAACGGATATTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACATCT 611
QY 601 AACATCTCTTTGAGGGTAAACATTTAGCAGAGCTGGTTCGAAAGATTTGTCAAGACAT 660
Db 612 AACATCTCTTTGAGGGTAAACATTTAGCAGAGCTGGTTCGAAAGATTTGTCAAGACAT 671
QY 661 TTTGCCCAATATCTCCGGGGTTTTCTCGTAGCTCCCATTCCTTCATATCTCAGCTCTTT 720
Db 672 TTTGCCCAATATCTCCGGGGTTTTCTCGTAGCTCCCATTCCTTCATATCTCAGCTCTTT 731
QY 721 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTAGAG 780
Db 732 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTGAAAAGGCCCTTTTAGAG 791
QY 781 AATCTTATTTCCAAATATTGACTCTCGAGGTCATTTCAGGAAGATTCAGTCACATGCTT 840
Db 792 AATCTTATTTCCAAATATTGACTCTCGAGGTCATTTCAGGAAGATTCAGTCACATGCTT 851
QY 841 ATATGAGAGCAGGAGCGCCAGCTCTCGACATGTGGAAGAGTGGTCCAGAAAGTGAAT 900
Db 852 ATATGAGAGCAGGAGCGCCAGCTCTCGACATGTGGAAGAGTGGTCCAGAAAGTGAAT 911
QY 901 ATACAAAAGTGGATTTCCAGGGAAAGTCCCAACCAAGATCAAGGATATCTGTGCAAT 960
Db 912 ATACAAAAGTGGATTTCCAGGGAAAGTCCCAACCAAGATCAAGGATATCTGTGCAAT 971
QY 961 AAAAGGAATGCTATATTGATAGAAATGAATGAGACCAACAGCTGGAGCCAGAGGCC 1020
Db 972 AAAAGGAATGCTATATTGATAGAAATGAATGAGACCAACAGCTGGAGCCAGAGGCC 1031
QY 1021 AGATCTATAAATGATAGAAAGCCCAAAATTTGCTGTGCTGTGGAACATATGATAT 1080
Db 1032 AGATCTATAAATGATAGAAAGCCCAAAATTTGCTGTGCTGTGGAACATATGATAT 1091
QY 1081 TATTATGCTCAACTTGTATGCTGAGGAGGAGGCCCAAAACCAAGTTATCACCTATT 1140
Db 1092 TATTATGCTCAACTTGTATGCTGAGGAGGAGGCCCAAAACCAAGTTATCACCTATT 1151
QY 1141 CCTCAAGAAATACCTGAGGATTTAGGATTTACGCTCAGGAAACAGGSCATGGTCCATCCCA 1200
Db 1152 CCTCAAGAAATACCTGAGGATTTAGGATTTACGCTCAGGAAACAGGSCATGGTCCATCCCA 1211
QY 1201 AGTCAATGSCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1260
Db 1212 AGTCAATGSCCTGCTGAGTACCTTCAGAGAAATTTGAAGCTCAACAATATAAGTTGAAA 1271
QY 1261 GTGGAGAGCAATTTGGGCTTCTGCTCCATCTTCTGCCGAGCCAAATTAACAACAGAGACAA 1320
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QY 421 ATGGTGGCAAGCTTGGGACCTTGGTATAGCAAGAGCTCTGAATATTTCCATGGAACCTT 480  
 Db |||||  
 QY 519 ATGGTGGCAAGCTTGGGACCTTGGTATAGCAAGAGCTCTGAATATTTCCATGGAACCTT 578  
 Db |||||  
 QY 481 GCTCGAAGCTTGTATTGGAACACCTTACTACCTGTCCCGAGAGATCTGTGAGAATAAACC 540  
 Db |||||  
 QY 579 GCTCGAAGCTTGTATTGGAACACCTTACTACCTGTCCCGAGAGATCTGTGAGAATAAACC 638  
 Db |||||  
 QY 541 TACACAATAAACAACGATATTGGTCTCTGGCTGTGCTTATATAGCTCTGACACAT 600  
 Db |||||  
 QY 639 TACACAATAAACAACGATATTGGTCTCTGGCTGTGCTTATATAGCTCTGACACAT 698  
 Db |||||  
 QY 601 AAACATCTCTTTGAGGGTAACAACCTTACAGAGCTGGTTCTGAAGATTGTCAAGACAT 660  
 Db |||||  
 QY 699 AAACATCTCTTTGAGGGTAACAACCTTACAGAGCTGGTTCTGAAGATTGTCAAGACAT 758  
 Db |||||  
 QY 661 TTGCCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGAATATCTCAGCTCTTT 720  
 Db |||||  
 QY 759 TTGCCCCAATATCTCCGGGGTTTCTCGTAGCTCCATTCCTTGAATATCTCAGCTCTTT 818  
 Db |||||  
 QY 721 CAAGTATCTCTCGAGACCGACCATCCATAATTCATTTTGAAGAGCCCTTTTATAG 780  
 Db |||||  
 QY 819 CAAGTATCTCTCGAGACCGACCATCCATAATTCATTTTGAAGAGCCCTTTTATAG 878  
 Db |||||  
 QY 781 AATCTATTCCCAATATTTGACTCCTGAGTCA--TTCAGGAAGAAATTCAGTCAATG 837  
 Db |||||  
 QY 879 AATCTATTCCCAATATTTGACTCCTGAGTCAAGTTTGAAGAGAAATTCAGTCAATG 938  
 Db |||||  
 QY 838 CTTATATCAGAGCAGGAGCGCCAGCTTCTGACATGCTGGAGAGTGGTCCAGAGTGT 897  
 Db |||||  
 QY 939 CTTATATCAGAGCAGGAGCGCCAGCTTCTGACATGCTGGAGAGTGGTCCAGAGTGT 998  
 Db |||||  
 QY 898 AAAATACAAAAAGTGAAGATTTCCAGGAAAGTCCCAAGATCAAGGATATCTGTGCCA 957  
 Db |||||  
 QY 999 AAAATACAAAAAGTGAAGATTTCCAGGAAAGTCCCAAGATCAAGGATATCTGTGCCA 1058  
 Db |||||  
 QY 958 ATTAAGAGATGCTATATTCATAGAAATGAATGGAGACACACAGCTGGAGCCAGAG 1017  
 Db |||||  
 QY 1059 ATTAAGAGATGCTATATTCATAGAAATGAATGGAGACACACAGCTGGAGCCAGAG 1118  
 Db |||||  
 QY 1018 GCAGATCTATAAAATGATAGAAAGCCCAAAATTTGCTGTCTGTGGACATTATGAT 1077  
 Db |||||  
 QY 1119 GCAGATCTATAAAATGATAGAAAGCCCAAAATTTGCTGTCTGTGGACATTATGAT 1178  
 Db |||||  
 QY 1078 TATTATTATGCTCAACTTGTATATGCTGAGAGAGAGCCCAAAACCAAGTTATCACCT 1137  
 Db |||||  
 QY 1179 TATTATTATGCTCAACTTGTATATGCTGAGAGAGAGCCCAAAACCAAGTTATCACCT 1238  
 Db |||||  
 QY 1138 ATTCCTCAAGAAATACTGGAGTTACGATGATGATGATGATGATGATGATGATGATGAT 1197  
 Db |||||  
 QY 1239 ATTCCTCAAGAAATACTGGAGTTACGATGATGATGATGATGATGATGATGATGATGAT 1298  
 Db |||||  
 QY 1198 CCAAGTCAATG 1208  
 Db |||||  
 QY 1299 CCAAGTCAATG 1309  
 Db |||||

RESULT 7  
 US-10-114-270-185  
 ; Sequence 185, Application US/10114270  
 ; Publication No. US20040030110A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Malyankar, Uriel M.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Liu, Zhaozhong  
 ; APPLICANT: Gusev, Vladimir Y.  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Zerhusen, Bryan D.

APPLICANT: Gorman, Linda  
 APPLICANT: Shenoy, Suresh G.  
 APPLICANT: Pena, Carol E.A.  
 APPLICANT: Smithson, Glenda  
 APPLICANT: Burgess, Catherine E.  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Padigar, Muralidhara  
 APPLICANT: Shimkets, Richard A.  
 APPLICANT: Gangolli, Esha A.  
 APPLICANT: Taupier Jr., Raymond J.  
 APPLICANT: Casman, Stacie J.  
 APPLICANT: Ji, Weizhen  
 APPLICANT: Anderson, David W.  
 APPLICANT: Liette, Mario W.  
 APPLICANT: Rastelli, Luca  
 APPLICANT: Edinger, Shlomit R.  
 APPLICANT: Stone, David J.  
 APPLICANT: MacDougall, John R.  
 APPLICANT: Rothenberg, Mark E.  
 TITLE OF INVENTION: No. US20040030110A1e1 Proteins and Nucleic Acids Encoding Same  
 FILE REFERENCE: 21402-322C  
 CURRENT APPLICATION NUMBER: US/10/114,270  
 CURRENT FILING DATE: 2002-11-27  
 PRIOR APPLICATION NUMBER: 60/281,086  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/281,136  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/281,863  
 PRIOR FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: 60/281,906  
 PRIOR FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: 60/282,020  
 PRIOR FILING DATE: 2001-04-06  
 PRIOR APPLICATION NUMBER: 60/282,930  
 PRIOR FILING DATE: 2001-04-10  
 PRIOR APPLICATION NUMBER: 60/282,934  
 PRIOR FILING DATE: 2001-04-10  
 PRIOR APPLICATION NUMBER: 60/283,512  
 PRIOR FILING DATE: 2001-04-12  
 PRIOR APPLICATION NUMBER: 60/283,710  
 PRIOR FILING DATE: 2001-04-13  
 PRIOR APPLICATION NUMBER: 60/284,234  
 PRIOR FILING DATE: 2001-04-17  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 470  
 SEQ ID NO 185  
 LENGTH: 1453  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(1198)  
 US-10-114-270-185

Query Match 57.4%; Score 1178.4; DB 16; Length 1453;  
 Best Local Similarity 99.2%; Pred. No. 1,1e-305;  
 Matches 1198; Conservative 0; Mismatches 1; Indels 9; Gaps 1;  
 QY 1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATCTTA 60  
 Db |||||  
 QY 1 ATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATCTTA 60  
 Db |||||  
 QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTTGAAGAATG 120  
 Db |||||  
 QY 61 GCTAAAGGGAATCAGATAGCAAGCACTGTGTCATAAAGAGATCAATTTTGAAGAATG 117  
 Db |||||  
 QY 121 CCATACAAAGAAAGAGAGCTTCAAGAAAGAGAGTATCTTCTCGAAAAGATGAAACAT 180  
 Db |||||  
 QY 118 -----CAAGAAAAAGAGCTTCAAGAAAGAGAGTATCTTCTCGAAAAGATGAAACAT 171  
 Db |||||  
 QY 181 CCCAACATTGTAGCTTCTTCAATTCTTCAAGAGAGATGGCAGGCTGTTTATTCTTAATG 240  
 Db |||||  
 QY 172 CCCAACATTGTAGCTTCTTCAATTCTTCAAGAGATGGCAGGCTGTTTATTCTTAATG 231  
 Db |||||

QY 241 GATATTTGATGGGGGATCTCATGAAAGGATCAATAGACAGGGGTGTATTT 300  
 Db |||||  
 QY 232 GATATTTGATGGGGGATCTCATGAAAGGATCAATAGACAGGGGTGTATTT 291  
 Db |||||  
 QY 301 AGTGAAGATCAGATCTCGTGGTGTGTACAGATTTCTTAGGACTAAACATATTCAT 360  
 Db |||||  
 QY 292 AGTGAAGATCAGATCTCGTGGTGTGTACAGATTTCTTAGGACTAAACATATTCAT 351  
 Db |||||  
 QY 361 GACAGGAAGATATACACAGGGGATCAATAGGATCAAGATTTCTTAGGAGACGGA 420  
 Db |||||  
 QY 352 GACAGGAAGATATACACAGGGGATCAATAGGATCAAGATTTCTTAGGAGACGGA 411  
 Db |||||  
 QY 421 ATGGTGGCAAGCTTGGGACATTTGTATAGCAAGAGTCTCTGAATATTCATGGAAT 480  
 Db |||||  
 QY 412 ATGGTGGCAAGCTTGGGACATTTGTATAGCAAGAGTCTCTGAATATTCATGGAAT 471  
 Db |||||  
 QY 481 GCTCGAATCTGTTTGGACACCTTACTACTGTCTCCAGAGATCTGTGAGATTAACCC 540  
 Db |||||  
 QY 472 GCTCGAATCTGTTTGGACACCTTACTACTGTCTCCAGAGATCTGTGAGATTAACCC 531  
 Db |||||  
 QY 541 TACAACAAATAAAGCGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACAT 600  
 Db |||||  
 QY 532 TACAACAAATAAAGCGATATTTGGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACAT 591  
 Db |||||  
 QY 601 AAACATCTTTTGGAGGTAAACACTTACAGCAGCTGGTCTCTGAAGATTTGTCAAGACAT 660  
 Db |||||  
 QY 592 AAACATCTTTTGGAGGTAAACACTTACAGCAGCTGGTCTCTGAAGATTTGTCAAGACAT 651  
 Db |||||  
 QY 661 TTTGGCCCAATATCTCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 Db |||||  
 QY 652 TTTGGCCCAATATCTCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 711  
 Db |||||  
 QY 721 CAAATATCTCTCGAGCAGCAGCATCCATAAATTCATTTTGAAGAGCCCTTTTAGAG 780  
 Db |||||  
 QY 712 CAAATATCTCTCGAGCAGCAGCATCCATAAATTCATTTTGAAGAGCCCTTTTAGAG 771  
 Db |||||  
 QY 781 AATCTTATCCCAATATTTGATCTCTGAGCTCAATTCAGGAGAAATTCAGTCAATGCT 840  
 Db |||||  
 QY 772 AATCTTATCCCAATATTTGATCTCTGAGCTCAATTCAGGAGAAATTCAGTCAATGCT 831  
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 QY 841 ATATGAGAGCAGGAGGCGGAGCTTCTGCACATGCTGGGAGAGTGGTCCAGAGGTAAA 900  
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 QY 832 ATATGAGAGCAGGAGGCGGAGCTTCTGCACATGCTGGGAGAGTGGTCCAGAGGTAAA 891  
 Db |||||  
 QY 901 ATACAAAAGTGAGATTCAGGAGAAAGTGGCCCAACCAAGATCAAGGATATCTGTGCAAT 960  
 Db |||||  
 QY 892 ATACAAAAGTGAGATTCAGGAGAAAGTGGCCCAACCAAGATCAAGGATATCTGTGCAAT 951  
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 QY 961 AAAGGAATGCTATATTTGCATAGAAATGAATGAGACCCAGCTGGAGCCAGAGGCC 1020  
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 QY 952 AAAGGAATGCTATATTTGCATAGAAATGAATGAGACCCAGCTGGAGCCAGAGGCC 1011  
 Db |||||  
 QY 1021 AGATCTATAAAAATGATAGAAAGCCCAAAATTTGCTGTGTGTGACATTAATGATAT 1080  
 Db |||||  
 QY 1012 AGATCTATAAAAATGATAGAAAGCCCAAAATTTGCTGTGTGTGACATTAATGATAT 1071  
 Db |||||  
 QY 1081 TATATGCTCAACTGATATGCTGAGGAGAGGCCCAACCAAGATTAATCAACCTAT 1140  
 Db |||||  
 QY 1072 TATATGCTCAACTGATATGCTGAGGAGAGGCCCAACCAAGATTAATCAACCTAT 1131  
 Db |||||  
 QY 1141 CCTCAAGAAATATCTGGAGTTGAGGATTAAGGTTCAGGAAACGAGGATGGTCCATCCCA 1200  
 Db |||||  
 QY 1132 CCTCAAGAAATATCTGGAGTTGAGGATTAAGGTTCAGGAAACGAGGATGGTCCATCCCA 1191  
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 QY 1201 AGTCAATG 1208  
 Db |||||  
 QY 1192 AGTCAATG 1199  
 Db |||||

RESULT 8  
 US-09-783-320-3  
 ; Sequence 3, Application US/09783320

; Patent No. US20020038011A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Hu, Yi  
 ; APPLICANT: Nepomnichy, Boris  
 ; APPLICANT: Turner, C. Alexander Jr  
 ; APPLICANT: Zambrowicz, Brian  
 ; TITLE OF INVENTION: No. US20020038011A1el Human Kinases and Polynucleotides Encoding  
 ; FILE REFERENCE: LEX-0137-USA  
 ; CURRENT APPLICATION NUMBER: US/09/783,320  
 ; CURRENT FILING DATE: 2001-02-15  
 ; PRIOR APPLICATION NUMBER: US 60/183,582  
 ; PRIOR FILING DATE: 2000-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/184,014  
 ; PRIOR FILING DATE: 2000-02-22  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 3645  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-783-320-3

Query Match 17.9%; Score 368; DB 9; Length 3645;  
 Best Local Similarity 66.0%; Pred. No. 1.3e-87;  
 Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;  
 QY 1 ATGATAGTACGATGTGATTAAGCCATCGGCAAGTGCCCTCGGGAAGCATACTTA 60  
 Db |||||  
 QY 1 ATGAGAGATATGTTAGACTACAGAAGATTGGAGAAGTTCAATTTGGAAGCCATCTT 60  
 Db |||||  
 QY 61 GCTAAGGGAATCAGATAGCAAGCAGTGTCTCTATAAAGAGATCAATTTTGAAGAGATG 120  
 Db |||||  
 QY 61 GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGATG 120  
 Db |||||  
 QY 121 CCCATACAGAAAAAGAGCTTCAAGAAAGAGAGTCTTCTGGAAGAGATCAACAT 180  
 Db |||||  
 QY 121 TCCAGTAAGAAAGAGAGAGATCAAGGAGAGAGTTGCGAGTATTTGGCAACATGAGCAT 180  
 Db |||||  
 QY 181 CCCAACATTTGAGCTTCTTCAATTTCAAGAGAAATGGCAGCTGTTTATTTGTAATG 240  
 Db |||||  
 QY 181 CCAATATTTGCCAGTATAGAGAAATCAATTTGAAGAAATGGCTCTCTACATAGTAATG 240  
 Db |||||  
 QY 241 GAATATTTGATGAGGGGATCTCATGAAAGGATCAATAGACAAACGGGTGTCTATTT 300  
 Db |||||  
 QY 241 GATTACTGTGAGGAGGGGATCTGTTTAAAGGAAATAATGCTCAGAAAGGCGTTTGT 300  
 Db |||||  
 QY 301 AGTGAAGATCAGATCTCGGTTGGTTTGTACAGATTTCTCTAGGACTAAACATATTCAT 360  
 Db |||||  
 QY 301 CAAGAGATCAGATTTTGGACTGGTTTGTACAGATATGTTTGGCCCTGAAACATGTACAT 360  
 Db |||||  
 QY 361 GACAGGAGATATTAACAGGAGATTAAGAGCTCAGAACATTTTCTTAGCAAGAGGA 420  
 Db |||||  
 QY 361 GATAGAAAAATTTCTCATCGAGACATTAATCTCAGAACATATTTTAACTAAAGATGGA 420  
 Db |||||  
 QY 421 ATGTTGGCAAGCTTGGGAGCTTTGGTATAGCAAGAGTCTGTAATAATTCATCGAACTT 480  
 Db |||||  
 QY 421 ACAGT---ACACTTGGAGATTTGGAAATGCTAGAGTTCTTAATAGTACTGTAGAGCTG 477  
 Db |||||  
 QY 481 GCTCGAATCTGTATTGGAACACCTTACTACTCTGCTGCCAGAGATCTGTGAGATAAACCC 540  
 Db |||||  
 QY 478 GCTCGAATCTGCATAGGAGCCCATCTACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537  
 Db |||||  
 QY 541 TACACATTAACCGGATATTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCACACTT 600  
 Db |||||  
 QY 538 TACATTAATAAAGTGACATTTGGGCTCTGGGGTGTGCTCTTTAGAGCTGTGTACACTT 597  
 Db |||||  
 QY 601 AAACATCTTTTGGAGGTAAACACTTACAGCAGCTGGTCTGTAAGATTTTGTCAAGCAT 660  
 Db |||||  
 QY 598 AAACATCTTTTGAAGCTGGCAGTATGAAGAAACCTGGTACTGAGATAAATATCTGGATCT 657  
 Db |||||  
 QY 661 TTTGCCCCAATATCTCGGGGTTTCTCGTGAGCTCCATTCCTTGATATCTCAGCTCTTT 720  
 Db |||||



534 ATGGAGAGTATGTTAGACTACAGAGATTTGGAGAGGTTTCATTTGGAAAGCCATTCCT 593  
QY 61 GCTAAAGGGAATCAGATAGCAGCAGCTGTGTCATATAAGAGATCAATTTTGAAGAATG 120  
Db 594 GTTAAATCTACAGAGATGGCAGCAGTATGTTATCAAGGAAATTAACATCTCAAGAATG 653  
QY 121 CCATACAGAGAAAGAGCTTCAAGAGAAAGAGTATCTTCTGGAAAGATGAACAT 180  
Db 654 TCCAGTAAAGAGAGAGAAATCAAGAGAGAGTTCAGTATTTGGCAACATGAAGCAT 713  
QY 181 CCAGCATTTGAGCCTTCTTCAATTCATTTCAAGAGAAATGGCAGGCTGTTTATGTAATG 240  
Db 714 CCAATATTGTCAGTATAGAGATCAATTTGAAGAAATGGCTCTCTACATAGTAATG 773  
QY 241 GAATATTGTCAGGAGGATCTCATGAAAGAGATCAATAGACAACAGGGGTGTTTATTT 300  
Db 774 GATTACTGTGAGGAGGAGATCTGTTAAGCGATTAATGCTCAAGAAAGCGTTTGT 833  
QY 301 AGTGAAGATCAGATCTCGTGGTGTGTTGACAGATTTCTTAGGATTAATAATTCAT 360  
Db 834 CAAGAGGATCAGATTTGGAGTGTGTTGACAGATATGTTGGCCCTGGAACATGTACAT 893  
QY 361 GACAGAGATATTACAGAGGACATATAAGCTCAGAACATTTTCTTAGCAGAACGGA 420  
Db 894 GATAGAAATCTTCATCGAGACATTAATCTCAGAACATATTTTAACTAAGATGGA 953  
QY 421 ATGGTGGCAAGAGCTTGGGAGCTTGGTATAGCAGAGTCTCTCAATAATTCATGGAAT 480  
Db 954 ACACTTGGAGATTTTGGAAATGCTAGAGTCTTAAATAGTACTGTAGAGCTG 1010  
QY 481 GCTCGAAGCTGTATTGGAACACCTTACTAGCTGTGCCAGAGATCTGTGAGAAATAACCC 540  
Db 1011 GCTCGAAGCTGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1070  
QY 541 TACAACAATAAAGAGATTTGGTCTCTTGGCTGTGTTTATATGAGCTCTGCACAT 600  
Db 1071 TACAATAATAAAGAGATTTGGGCTCTGGGCTGTGCTTATGAGCTGTGACAT 1130  
QY 601 AAACATCTTTGAGGATTAACATTTACAGAGCTGGTCTGAAAGATTTGTCAAGACAT 660  
Db 1131 AAACATGCTTTGAGAGCTGGCAGTATGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190  
QY 661 TTGCCCCAATATCTCGGGGTTTCTCGTGAGCTCCATCTCTGATATCTCAGCTCTTT 720  
Db 1191 TTTCACCTGTGCTTTGCAATTAATCCTATGATCTCCGAGTGTGTTGCTCAGTTAT 1250  
QY 721 CAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGGCGCTTTTAGAG 780  
Db 1251 AAAAGAAATCTTAGGATAGACCATCAGTCACTCCATATTTGGAGAAAGGTTTATAGCC 1310  
QY 781 AATCTTATCCCAATATTGACTCTGAGTCAATTCAGAGAGATTCAGTC 832  
Db 1311 AAACGCAATGAAAGTTTCTCTCTCCTCAGCTTATTCAGAGAAATTTTGTG 1362

## RESULT 11

US-10-117-722-246  
; Sequence 246, Application US/10117722  
; Publication No. US20030219744A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2BCIP  
; CURRENT APPLICATION NUMBER: US/10/117,722  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/520,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: pt FL genes Version 1.0  
; SEQ ID NO 246  
; LENGTH: 5448  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (534)..(4178)  
US-10-117-722-246

Query Match 17.9%; Score 368; DB 15; Length 5448;  
Best Local Similarity 66.0%; Pred. No. 1.7e-87;  
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 1 ATGGATAGTACGATGTGATTAAGGCCATCGGCAAGTGCCTTCGGGAAAGCATACTTA 60  
Db 534 ATGGAGAGTATGTTAGACTACAGAGATTTGGAGAGGTTTCATTTGGAAAGCCATTCCT 593  
QY 61 GCTAAAGGGAATCAGATAGCAGCAGCTGTGTCATATAAGAGATCAATTTTGAAGAATG 120  
Db 594 GTTAAATCTACAGAGATGGCAGCAGTATGTTATCAAGGAAATTAACATCTCAAGAATG 653  
QY 121 CCCATACAGAGAAAGAGCTTCAAGAGAAAGAGTATCTTCTGGAAAGATGAACAT 180  
Db 654 TCCAGTAAAGAGAGAGAAATCAAGAGAGAGTTCAGTATTTGGCAACATGAAGCAT 713  
QY 181 CCCAAGATTTGAGCCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGTTTATGTAATG 240  
Db 714 CCAATATTGTCAGTATAGAGATCAATTTGAAGAAATGGCTCTCTACATAGTAATG 773  
QY 241 GAATATTGTCAGGAGGATCTCATGAAAGAGTCAATAGACAACGGGTGTTTATTT 300  
Db 774 GATTACTGTGAGGAGGAGGATCTGTTAAGCGATTAATGCTCAGAAAGCGTTTGT 833  
QY 301 AGTGAAGATCAGATCTCGTGGTGTGTTGACAGATTTCTTAGGATTAATAATTCAT 360  
Db 834 CAAGAGGATCAGATTTGGAGTGTGTTGACAGATATGTTGGCCCTGGAACATGTACAT 893  
QY 361 GACAGAGATATTACAGAGGACATATAAGCTCAGAACATTTTCTTAGCAGAACGGA 420  
Db 894 GATAGAAATCTTCATCGAGACATTAATCTCAGAACATATTTTAACTAAGATGGA 953  
QY 421 ATGGTGGCAAGAGCTTGGGAGCTTGGTATAGCAGAGTCTCTCAATAATTCATGGAAT 480  
Db 954 ACACTTGGAGATTTTGGAAATGCTAGAGTCTTAAATAGTACTGTAGAGCTG 1010  
QY 481 GCTCGAAGCTGTATTGGAACACCTTACTAGCTGTGCCAGAGATCTGTGAGAAATAACCC 540  
Db 1011 GCTCGAAGCTGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1070  
QY 541 TACAACAATAAAGAGATTTGGTCTCTTGGCTGTGTTTATATGAGCTCTGCACAT 600  
Db 1071 TACAATAATAAAGAGATTTGGGCTCTGGGCTGTGCTTATGAGCTGTGACAT 1130  
QY 601 AAACATCTTTGAGGATTAACATTTACAGAGCTGGTCTGAAAGATTTGTCAAGACAT 660  
Db 1131 AAACATGCTTTGAGAGCTGGCAGTATGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190  
QY 661 TTGCCCCAATATCTCGGGGTTTCTCGTGAGCTCCATCTCTGATATCTCAGCTCTTT 720  
Db 1191 TTTCACCTGTGCTTTGCAATTAATCCTATGATCTCCGAGTGTGTTGCTCAGTTAT 1250  
QY 721 CAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGAGGCGCTTTTAGAG 780  
Db 1251 AAAAGAAATCTTAGGATAGACCATCAGTCACTCCATATTTGGAGAAAGGTTTATAGCC 1310  
QY 781 AATCTTATCCCAATATTGACTCTGAGTCAATTCAGAGAGATTCAGTC 832  
Db 1311 AAACGCAATGAAAGTTTCTCTCTCCTCAGCTTATTCAGAGAAATTTTGTG 1362

```
RESULT 12
US-10-037-270-245
; Sequence 245, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)..(4262)
US-10-037-270-245

Query Match 17.9%; Score 368; DB 15; Length 5532;
Best Local Similarity 66.0%; Pred. No. 1.7e-87;
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 1 ATGGATAAGTACGATGTGATTAGGCGCATCGGGCAAGTCTTCGGGAAAGCATCTTA 60
DB 534 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTTCATTTGGAAAGCCATCTT 593
QY 61 GCTAAAGGAAATCAGATAGCAAGCACTGTGTCTATTAAGAGATCAATTTTGAAGAATG 120
DB 594 GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGATG 653
QY 121 CCATACAGAAAAGAGCTTCAAGAAAGAGTATCTTCGGAAGATGAACAT 180
DB 654 TCCAGTAAAGAAGAGAGAAGATCAAGGAGAGAGTTGAGTATGGCAACATGAGCAT 713
QY 181 CCCAATTTGTAGCCCTCTTCAATTCATTTCAAGAGAAATGGCAGCTGTTTATTGTAATG 240
DB 714 CCAATATTTGCCAGTATAGAGATCAATTTGAAGAAATGCTCTCTCTCATAGTAATG 773
QY 241 GAATATTGTAGTGGAGGGATCTCATGAAGAAGATCATATACACAGGGGTGTGTTATT 300
DB 774 GATTACTGTGAGGAGGGGATCTGTTAAGCGAATAAATGTCAGAAAGGGGTGTTGTT 833
QY 301 AGTGAAGATCAGATCTCGGTGGTGTGTACAGATTTCTTAGGATAAAACATATTCAT 360
DB 834 CAAGAGGATCAGATTTTGGACTGGTTTGTACAGATATGTTTGGCCCTGAACATGTACAT 893
QY 361 GACAGGAAGATATTACACAGGAGACATAAAGCTCAGAACATTTTCTTAGCAAGACGA 420

894 GATAGAAAATTTCTTCATCGAGACATTAATCTCAGACATATTTTAACATAAGATGA 953
421 ATGGTGCAAAAGTTTGGGACTTTGTGTATAGCAAGAGTCTCTGAATAATTTCCATGGAATT 480
954 ACAGT--ACAACCTTGGAGATTTTGGAAATTTGCTAGAGTTCTTAAATAGTACTGTAGAGCTG 1010
481 GCTCGAACTTGTATTGGAACACCTTACTACTCTGCCAGAGATCTGTGAGATAAACC 540
1011 GCTCGAACTTGTATAGGACCCCACTACTTGTGACCTGAATCTGTGAAAACAAACCT 1070
541 TACAACAATAAAACGGATATTTGGTCTCTTGGCTGTGTCTTATATAGCTCTGCACTT 600
1071 TACAATAATAAAAGTGACATTTGGGCTCTGGGCTGTGCTCTTATGAGCTGTGACATT 1130
601 AARACATCTTTTGGAGGTACAACTTTACAGACAGTGGTCTCGAAGATTTGTCAAGCACAT 660
1131 AAACATGCTTTTGAAGCTGGCAGTATGAAAACCTTGTAAGTATATCTGGAATCT 1190
661 TTTGCCCAATATCTCCGGGGTTTTCTCGTGAAGTCCATTCCTTGATATCTCAGCTCTTT 720
1191 TTTCCACCTGTGTCTTTGCAATTTCTCTATGATCTCCGCAAGTTTGTGTCTCAGTTATT 1250
721 CAGATATCTCTCGACACCGACCATTCATAAATTCATTTTGAAGAGGCCCTTTTAGAG 780
1251 AAAAGAAATCTAGGATAGACCATCAGTCAACTCCATATTTGGAGAAAGGTTTATAGCC 1310
781 AATCTTATTTCCCAATATTTGACTCTCTGAGGTCAATTCAGGAAGAATTCAGTC 832
1311 AAACGCAATTGAAAAGTTTCTCTCTCTCAGCTTATTCAGAGAAGATTTTGTGTC 1362

RESULT 13
US-10-117-722-245
; Sequence 245, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (534)..(4262)
US-10-117-722-245

Query Match 17.9%; Score 368; DB 15; Length 5532;
Best Local Similarity 66.0%; Pred. No. 1.7e-87;
Matches 549; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 1 ATGGATAAGTACGATGTGATTAGGCGCATCGGGCAAGTCTTCGGGAAAGCATCTTA 60
DB 534 ATGGAGAAGTATGTTAGACTACAGAAGATTGGAGAAGGTTTCATTTGGAAAGCCATCTT 593
QY 61 GCTAAAGGAAATCAGATAGCAAGCACTGTGTCTATTAAGAGATCAATTTTGAAGAATG 120
DB 594 GTTAAATCTACAGAAGATGGCAGACAGTATGTTATCAAGGAAATTAACATCTCAAGATG 653
QY 121 CCATACAGAAAAGAGCTTCAAGAAAGAGTATCTTCGGAAGATGAACAT 180
DB 654 TCCAGTAAAGAAGAGAGAAGATCAAGGAGAGAGTTGAGTATGGCAACATGAGCAT 713
QY 181 CCCAATTTGTAGCCCTCTTCAATTCATTTCAAGAGAAATGGCAGCTGTTTATTGTAATG 240
DB 714 CCAATATTTGCCAGTATAGAGATCAATTTGAAGAAATGCTCTCTCTCATAGTAATG 773
QY 241 GAATATTGTAGTGGAGGGATCTCATGAAGAAGATCATATACACAGGGGTGTGTTATT 300
DB 774 GATTACTGTGAGGAGGGGATCTGTTAAGCGAATAAATGTCAGAAAGGGGTGTTGTT 833
QY 301 AGTGAAGATCAGATCTCGGTGGTGTGTACAGATTTCTTAGGATAAAACATATTCAT 360
DB 834 CAAGAGGATCAGATTTTGGACTGGTTTGTACAGATATGTTTGGCCCTGAACATGTACAT 893
QY 361 GACAGGAAGATATTACACAGGAGACATAAAGCTCAGAACATTTTCTTAGCAAGACGA 420
```

Db 594 GTTAAATCTACAGAGATGGCAGAGATGTTATCAAGAAATTAACATCTCAAGATG 653  
QY 121 CCCATCAAGAAAGAAAGCTTCAAGAAAGAGTATCTTCTGAAAGAGTAAACAT 180  
Db 654 TCCAGTAAAGAGAGAGAGATCAAGAGAGAGTTCAGATTTGGCAACATGAGCAT 713  
QY 181 CCCACATTTAGCTTCTTCAATTCATTTCAAGAGATGCGAGGCTGTTTATGTAATG 240  
Db 714 CCAATATTTGTCAGATATAGAGATCAATTTGAAGAAATGCGCTCTCTACATAGTAATG 773  
QY 241 GAATATTGTATGGAGGATCTCATGAAAGAGATCAATAGACAAAGGGGTGTTATTT 300  
Db 774 GATTACTGTGAGGAGGAGATCTGTTTAGCGAATAATGCTCAGAAAGGGGTTTGT 833  
QY 301 ACTGAAGATPCAGATCCTCGTTGTTGTGATGATTTCTTAGGACTAAACATATTCAT 360  
Db 834 CAAGAGGATCAGATTTGGACTGTTTGTACAGATATGTTTGGCCCTGAAACATGTACAT 893  
QY 361 GACAGGAAGATATTACAGAGGACATATAAGCTCAGAACATTTTCTTAGCAGAACGGA 420  
Db 894 GATAGAAAATTCCTCATCGAGACATTAATCTCAGAACATATTTTAACTAAAGATGGA 953  
QY 421 ATGGTGGCAAGACTTGGGACATTTGGTATAGCAAGAGTCCCTGAATAATTCATGAACTT 480  
Db 954 ACAGT---ACACTTGGAGATTTTGGATTTGCTAGATTTCTTAATAGTACTGTAGAGCTG 1010  
QY 481 GCTCAACTTGTATTGGAAACCTTACTACCTGTCCAGAGATCTGTCAAGATTAACCC 540  
Db 1011 GCTCAACTTGTATAGGAGCCCATCTACTCTGACCTGAAATCTGTGAAAACAAACCT 1070  
QY 541 TACAACAATAAAGAGATTTGGTCTCTTGTGCTGTCTTATATGAGCTCTGCACATTT 600  
Db 1071 TACAATAATAAAGTGACATTTGGGCTCTGGGCTGTGCTTATGAGCTGTGACATTT 1130  
QY 601 AAACATCTTTTGGGGTAAACATTAACAGAGCTGGTCTGAAAGATTTGTCAGACAT 660  
Db 1131 AAACATGCTTTTGAAGCTGGCAGTATGAAACCTGGTACTGAAGATAATATCTGGATCT 1190  
QY 661 TTTGCCCCAATATCTCCGGGTTTCTGCTGAGCTCCATCTCTTATATCTCAGCTCTTT 720  
Db 1191 TTTCCACCTGTGCTCTTGCATTTATTCCTATGATCTCCGAGTTTGGTGTCTCAGTTATT 1250  
QY 721 CAAGTATCTCTCGAGACGACATCCATAATTCATTTTGAAAGGCCCTTTTAGAG 780  
Db 1251 AAAAGAAATCTTAGGATAGACCATCAGTCACTCCATTTGGAGAAAGTTTATAGCC 1310  
QY 781 AATCTTATCCAAATATTGACTCCTGAGGTCATTCAGGAAGAATTCAGTC 832  
Db 1311 AAACGCAATGAAAAGTTTCTCTCTCCTCAGCTTATTCAGAGAAGATTTTGTGTC 1362

RESULT 14

US-10-114-270-183  
; Sequence 183, Application US/10114270  
; Publication No. US20040030110A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Malyenkar, Uriel M.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Liu, Zhaozhong  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Li, Li  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Smithson, Glennnda  
; APPLICANT: Burgess, Catherine E.

; APPLICANT: Gerlach, Valerie  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Anderson, David W.  
; APPLICANT: Liete, Mario W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Stone, David J.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Rothenberg, Mark E.  
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-322C  
; CURRENT APPLICATION NUMBER: US/10/114,270  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/281,086  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,020  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,930  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,512  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SEQ ID NO 183  
; LENGTH: 1588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (246)..(1521)  
; US-10-114-270-183

Query Match 12.7%; Score 260.8; DB 16; Length 1588;  
Best Local Similarity 59.0%; Pred. No. 5.3e-59;  
Matches 486; Conservative 0; Mismatches 332; Indels 6; Gaps 2;

QY 1 ATGGATAAGTACGATGTGATTAAAGCCATCGGCAAGGTGCCTTCGGAAAGCATACTTA 60  
Db 246 ATGGATGACTACATGTGCTCTGAGAATGATTGGGAGGGCTCTCTTCGGCAGAGCTCTTTG 305  
QY 61 GCTAAAGGGAAATCAGATAGCAAGCACTGTGTCTATAAAGAGATCAATTTTGAAGATG 120  
Db 306 GTTCAGCATGAAGCAGTATCAGATGTTGCCATGAAGAATAGGCTTCCCAAGGTC 365  
QY 121 CCATACAGAAAAAGAGCTTCAAGAAAGAGTATTTCTTGGAAAAAGATGAACAT 180  
Db 366 ACTACTAATACACAGAA---TTCTAGAGAGGAGGCTGTTCTTTTAGCCAAAATGAAACAC 422  
QY 181 CCCAACATTTAGCTTCTTCAATTCATTTTCAAGAGATGCGAGGCTGTTTATTGTAATG 240  
Db 423 CCTAATATTGTTGCCCTTCAAGAAATCATTTGAAGCTGAGGACACTTGTATATTGTATG 482  
QY 241 GAATATTGTATGAGGGGATCTCATGAAAGGATCAATAGACACCGGGGTGTGTTATT 300  
Db 483 GAATACTGTATGAGGGGATCTAATGCAAAAGATTAAACAGCAGAGAAAGAAAGTTATT 542



301 AGTGAAGATCAGATCCTCGGTTGGTTGTACAGATTTCTTAGCACTAAACATATTCAT 360  
|||||  
543 CTTGAAGACAGATTAATTTGGTTTACCCAAATGTGCTTGGAGTAATCACATTCAC 602  
|||||  
361 GACGGAAGATATTACACAGGACATAAAGCTGAGAACATTTTCTTAGCAAGACGGA 420  
|||||  
603 AAGAAACGTGTGCTACACAGAGATATCAAGTCCAGATATCTTCCCTCACTCAGAATGGA 662  
|||||  
421 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGTCCTGAATAATTCATCGAACTT 480  
|||||  
663 AAGTG---AAATTGGGAGACTTTGGATCTGCCGTCTCCTCTCCAATCCGATGCCATTT 719  
|||||  
481 GCTCGAATCTGATTGGAACACCTTACTACCTGTGCTCCCGAGAGATCTGTGAGAAATTAACCC 540  
|||||  
720 GCTTGTACCTATGTGGGAACCTCTTATTATGTGCTCCAGAAATTTGGGAAACCTGCT 779  
|||||  
541 TACACATATAACCGATATTGGTCTCTTGGCTGTGCTTATATGAGCTCTGCACACTT 600  
|||||  
780 TATAACAATAAAGTGACATCTGGTCTTGGTGTGATCTCTGATGAATCTGTACCTT 839  
|||||  
601 AAACATCTTTTGGAGGTAACAACCTACAGCAGCTGTTCTTGAAGATTTGTCAAGACAT 660  
|||||  
840 AAGCATCCATTTCAGGCAATAGTTGGAAATATCTTATCTCAAGATATGTCAAGGTGC 899  
|||||  
661 TTTGCCCAATATCTCCGGGTTTCTCGTGAAGCTCCTTCTTGATATCTCAGCTCTT 720  
|||||  
900 ATCAGTCCACTGCGCTCATCTACTCTTGAATTCAGTTCTCTAGTCAAGCAGATGTT 959  
|||||  
721 CAAGTATCTCTCGAGACCGACCATCCATAAATTCATTTTGAAGGCGCTTTTGAAG 780  
|||||  
960 AAGGAATCTCTACATCGCCCTCGCTACAGGCTTCTCTCGAGGATCTGTAGCT 1019  
|||||  
781 AATCTTATCCCAATATTGACTCTCTGAGTCAATTCAGGA 824  
|||||  
1020 CGGCTGTCCAGAGTGTCTTACCCCGAGATCATCATGGAATA 1063  
|||||

RESULT 15

US-10-114-270-181  
; Sequence 181, Application US/10114270  
; Publication No. US20040030110A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Liu, Zhaozhong  
; APPLICANT: Gusev, Vladimir V.  
; APPLICANT: Li, Li  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Anderson, David W.  
; APPLICANT: Liete, Mario W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Stone, David J.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Rothenberg, Mark E.  
; TITLE OF INVENTION: No. US20040030110A1e1 Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-322C  
; CURRENT APPLICATION NUMBER: US/10/114,270  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/281,086  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,020  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,930  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,512  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SEQ ID NO 181  
; LENGTH: 1781  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (246)..(1713)  
US-10-114-270-181

Query Match 12.6%; Score 259.2; DB 16; Length 1781;  
Best Local Similarity 58.9%; Pred. No. 1.5e-58;  
Matches 485; Conservative 0; Mismatches 333; Indels 6; Gaps 2;

QY 1 ATGGATAGTACGATGTGATTAAGGCCATCGGCAAGTGGCTTCGGGAAAGCATACTTA 60  
Db 246 ATGGATAGTACGATGTGCTGAGATGATTTGGGAGGCTCTCTCGGAGAGCTCTTTTG 305  
QY 61 GCTAAAGGGAATCAGATAGCAAGCAGCTGTGTCTATAAAGAGATCAATTTGAAAGATG 120  
Db 306 GTTCAGCATGAAAGCAGTAATCAGATGTTTGCATGAAAGAAATTAAGGCTTCCCAAGTC 365  
QY 121 CCCATCAAGAAAGAGAGCTTCAAGAAAGAGTATCTTCTCGAAAGAGTGAACAT 180  
Db 366 ACTACTAATACACAGAA---TTCTAGGAAGGAGGCTGTCTTTTAGCAAAATGAACAC 422  
QY 181 CCCAATTTGTAGCCTTCTTCAATTCATTTCAAGAGATGGCAGGCTGTTTTATGTAATG 240  
Db 423 CCTAATTTGTTCCTTCAAGAAATCAATTTGAAGCTGAAGGACACTTGTATATTGTGATG 482  
QY 241 GAATATTGTATGGAGGGATCTCATGAAAGATCAATAGACACGGGTGTGTTATTT 300  
Db 483 GAATACTGTATGGAGGGATCTAATGCAAAAGATTTAAACAGCAAGAAAGGAAATTTT 542  
QY 301 AGTGAAGATCAGATCCTCGTTTGTGTTGTACAGATTTCTTAGGACTAAACATATTCAT 360  
Db 543 CTTGAAGACAGATACTTAATTTGTTTACCBAATGTGCTTGGAGTAAATCACATTCAC 602  
QY 361 GACAGGAAGATATTACACAGGACATAAAGCTGAGACATTTTCTTAGCAAGACGGA 420  
Db 603 AAGAAACGTGTGCTACACAGAGATATCAAGTCCAGAAATATCTTCTCACTCAGAATGGA 662  
QY 421 ATGGTGGCAAGCTTGGGACTTTGGTATAGCAAGAGCTCTGTAATTAATTCATGAACTT 480  
Db 663 AAGTG---AAATTGGGAGACTTTGGATCTGCCGTCTCCTCTCCAATCCGATGCCATTT 719  
QY 481 GCTCGAATCTGATTGGAACACCTTACTACCTGTCCCGAGAGATCTGTGAGAAATTAACCC 540  
Db 720 GCTTGTACCTATGTGGGAACCTCTTATTATGTGCTCCAGAAATTTGGGAAACCTGCT 779



